

# Search Report

#### STIC Database Tracking Number: 2287

To: PATRICIA DUFFY

Location: REM-3B05 / Mailbox 3C18

Art Unit: 1645

Thursday, June 28, 2007

Case Serial Number: 09/955502

From: HUGH YOUNG

**Location: EIC 1600** 

REM-1D58 / REM-1A64 Phone: (571)272-5722

hugh.young2@uspto.gov

#### **Search Notes**

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Hugh P. Young Ph.D. ASRC Management Services USPTO Contractor/EIC1600



STIC-Biotech/ChemLib Duffy, Patricia From: Friday, June 22, 2007 6:24 PM Sent: STIC-Biotech/ChemLib To: Subject: sequence search Importance: High IN RE:09/955,502 Please search SEQ ID NO:11. Please include a commercial and interference database search. Please PRINT OUT top 25 hits and deliver to examiner. Patricia A. Duffy, Ph.D. Primary Patent Examiner 571-272-0855, Remsen 3B05 Mailbox: 3C18 \*\*\*\*\*\*

Type of Search

NA#\_\_\_\_\_ AA#:\_\_

Encode/Transl:\_\_\_\_\_

S/L:\_\_\_\_ Oligomer:\_\_\_

Structure #:\_\_\_\_Text:\_

Inventor:\_\_\_\_ Litigation:\_\_\_

Searcher:

Searcher Phone:\_

Date completed:\_\_

Date Searcher Picked up:\_

Online Time:

Searcher Prep Time:

SEQUENCE SYSTEM:\_\_\_\_\_
WWW/Internet:\_\_\_\_
Other (Specify):\_\_\_\_

Vendors and cost where applicable

STN:\_\_\_\_

QUESTEL/ORBIT:\_\_\_

LEXIS/NEXIS:\_

DIALOG:\_

GenCore version 6.2.1 (c) 1993 - 2007 Biocceleration Ltd. Copyright

protein search, using sw model OM protein

Run on:

Search time 39 Seconds (without alignments) 224.506 Million cell 2007, 11:05:06 June 27,

updates/sec

91

US-09-955-502A-11 486 1 MSRTIFCTFLQREAEGQDFQ......NFLFEGKEVHIEGYTPEDKK score: Title: Perfect sc Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext

0.5

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 2000000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

•• Database

PIR 80: \*
2: pir1: \*
3: pir2: \* 4 0 m 4

pir4:\*

printed Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being pand is derived by analysis of the total score distribution.

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## ALIGNMENTS

Ageories: Escherichia coli
C;Species: I6-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004
C;Accession: A85594.
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Recession: A8554
A;Residues: 1-91 <STO>
A;Residues: Strain O157:H7, Substrain EDL933
C;Genetics:
A;Gene: yggX
C;Superfamily: fe(II) trafficking protein YggX
C;Superfamily: fe(II) trafficking protein YggX

Score 486; 100.0%;

Length 91;

DB 2;

Query Match

Thu

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Conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica serovar Typhi
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C;Accession: AH0879
C;Accession: AH0870
C;Accesi
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8train N16961; biotype El Tor
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.; Qin, H.; Dragoi, I.;
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C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_
C;Accession: C82320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W.C.; Clayton, F
in, J.; Bass, S.;
Fraser, C.M.
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PMID:10952301
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Pred. No. 7.9e-40;
5; Mismatches 0;
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Pred. No. 3.6e-33;
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A; Title: DNA Sequence of both chromosomes of the A; Reference number: A82035; MUID: 20406833; PMID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            d. No. 3.66
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A;Cross-references: UNIPARC:UPI0000C2CCF
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Similarity 94.5%;
86; Conservative
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A;Residues: 1-91 <PAR>
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Superfamily: fe(II)
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C, Superfamily: fo
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C;Superfamily:
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C; Species: Escherichia coli
C; Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C; Accession: F91108
R; Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A; Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H
A; Reference number: A99629; MUID:21156231; PMID:11258796
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-91 < HAY>
A; Residues: 1-91 < HAY>
A; Residues: 1-91 < HAY>
A; Experimental source: strain O157:H7, substrain RIMD 0509952
C; Genetics:
A; Genetics:
C; Superfamily: fe(II) trafficking protein YggX
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                                                                                                                                                                                                                                                                                                                                                     hypothetical protein b2962 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Species: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oc
C;Accession: A65082
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland
A; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65082
A;Accession: A65082
A;Accession: A65082
A;Kesidues: 1-91 < BLAT>
A;Residues: 1-91 < BLAT>
A;Residues: 1-91 < BLAT>
C;Superimental source: strain K-12, substrain MG1655
C;Superfamily: fe(II) trafficking protein YggX
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                                                                                         th 100.0%; Score 486; DB 2; Length 91; Similarity 100.0%; Pred. No. 1.6e-41; 91; Conservative 0; Mismatches 0; Indels
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llarity 100.0%; Pred. No. 1.6e-41;
Conservative 0; Mismatches 0;
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                                            Mismatches
                                                                                                                                                                                            61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK
                       Pred. No.
 100.08; Pt
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                                               Conservative
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                    Similarity
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conserved hypothetical protein XF1908 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C;Accession: C82624
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aeruginosa (strain_PAO1)
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                                                                                                                                                                                                                Buchnera
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A.; Larbig,
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hypothetical protein [imported] - Buchnera sp. (strain APS)
C; Species: Buchnera sp.
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-20
C; Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-20
C; Accession: E84994
R; Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A; Title: Genome sequence of the endocellular bacterial symbiont of aphids A; Reference number: A84930; MUID: 20445173; PMID: 10993077
A; Accession: E84994
A; Accession: E84994
A; Cross-references: UNIPARC: UPI000005E610; GB: AP000398; GSPDB: GN00144
A; Experimental source: strain APS
C; Genetics:
A; Genetics:
A; Genetics:
C; Superfamily: fe(II) trafficking protein YggX
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C;Species: Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-;
C;Accession: H83003
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; .; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opp A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opp A;Accession: H83003
A;Accession: H83003
A;Accession: H83003
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <STO>
A;Cross-references: UNIPARC:UPI00000C5F26; GB:AE004927; GB:AE004091; NII
C;Genetics:
A;Gene: PA5148
C;Guperfamily: fe(II) trafficking protein YggX
                                                                               05-Oct
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32;
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Pred. No. 1.6e-19
16; Mismatches 1
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Pred. No. 3.7e-16
10; Mismatches 33
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61.8%;
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Best Local Similarity 61.8
Matches 47; Conservative
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nes 45; Conser
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Best Local S
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                                                                                                                                                                                                 C; Species: Yersinia pestis
C; Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C; Accession: Al0116
R; Parkhill; J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A; Tatus: preliminary
A; Accession: Al0116
A; Status: preliminary
A; Molecule type: DNA
A; Creferences: UNIPARC: UP10000DCCC4; GB: AL590842; PIDN: CAC89796.1; PID: g15979022; C; Genetics:
A; G
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C;Species: Haemophilus influenzae
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C;Accession: C64013
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64013
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-90 <TIGR>
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A;Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32'
C;Superfamily: fe(II) trafficking protein YggX
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Best Local Similarity 82.2%; Pred. No. 1.4e-32;
Matches 74; Conservative 8; Mismatches 8;
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K.E.; Eisen, Dougherty, B Pizza, M.

19-Jan-2001

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NID:97226857;

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NID:97380371;

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Neisseria meningitidis (strain MC58
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C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C;Accession: A81807
C;Accession: A81807
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Raj Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81807
A;Accession: A81807
A;Accession: A81807
A;Actus: preliminary
A;Molecule type: DNA
A;Residues: 1-546 <PAR>A;Cross-references: UNIPARC:UPI00000C4CA5; GB:AL162757; GB:AL157959; NID:g738037
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                                                                                                                                                                                             MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2;Accession: C81063
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GB:AE002098;
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MC58
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Z2491
                                                                                                                  .4;
33;
                                                                                Score 213; DB 2;
Pred. No. 2.2e-14
; Mismatches 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: serogroup o, control C; Genetics:
A; Gene: NMB1613
C; Superfamily: iron-dependent fumarate hydratase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: iron-dependent fumarate hydratase;
Keywords: carbon-oxygen lyase; hydro-lyase
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Pred. No.
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                                                                                                                                                                                                                                                                                                              EHRKLLEQEMVNFLFEGKEVHIEGYTPE
                                                                                                                                                                                                                                                                                                                                                                    61 RAREYLAQQMEQYFFGDGADAVQGYVPQ
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30.2%;
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Similarity 44.3%;
39; Conservative 1
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19; Conser
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Molecule type
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Best Local S
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A; Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; V A; Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A; Reference number: A81000; MUID:20175755; PMID:10710307
A; Reference number: A81000; MUID:20175755; PMID:10710307
A; Residues: 1-88 *TETP
A; Residues: 1-88 *TETPP
A; Residues: 1-88 *TETPP
A; Residues: 1-88 *TETPP
A; Residues: 1-88 *TETPP
A; Residues: 1-89 *TETPP
A; Residues: 1-80 *TETPP
A; Re
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Rajandream,
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strain MC58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 MQRIIFCEYEQRDTEGLDFVPYPGELGQKIFACIGKVGWAAWLVHQTMLINENRLSPRNP
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A;Gene: XF1908
C;Superfamily: f
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Best Local S
Matches 45
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09-Jul-2004
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M.; Yasuda, I
                                                                                                                                                                                                                                                                                                                                                   Residues: 1-2488 <STE>Cross-references: UNIPROT:O61528; UNIPARC:UPI0000611F8; EMBL:AF048834; ACCESSION: T42740
Status: preliminary; translated from GB/EMBL/DDBJ
Molecule type: mRNA
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                                                                                                                                                                                                     Cell 92, 785-795, 1998
A;Title: UNC-73 activates the Rac GTPase and is required for A;Reference number: Z22256; MUID: 98188103; PMID: 9529254
A;Accession: T42739
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                                                                                                            Caenorhabditis
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A; Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena C; Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_chargesion: AC2256
R; Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamotc Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamac
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Residues: 1-1634,'ON',1637,'E' <ST2>
Cross-references: UNIPARC:UPI000002A21C; EMBL:AF048835;
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A;Map position: I
A;Introns: 7/3; 64/2; 95/3; 230/3; 265/2; 335/3; 360/3; 4
19/3; 2262/2; 2331/1; 2351/3; 2396/1; 2431/1
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Residues: 'MVIKCFT',1568,'LRK',1572-2488 <DU3>
Cross-references: UNIPARC:UPI000002A21D; EMBL:U80436;
Experimental source: strain Bristol N2; clone F55C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Residues: 1-1634,'QN',1637,'E' <DU2>
Cross-references: UNIPARC:UPI000002A21C; EMBL:U80436;
Experimental source: strain Bristol N2; clone F55C7
Accession: T34426
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submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid F55C7
A;Reference number: Z21524
A;Reference number: T34427
A;Accession: T34427
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C;Species: Caenorhabditis elegans
C;Date: 11-Jan-2000 #sequence revision 11-Jan-2000 #
C;Accession: T42739; T42740; T34427; T34430; T34426
C;Accession: T42739; T42740; T34427; T34430; T34426
R;Steven, R.; Kubiseski, T.J.; Zheng, H.; Kulkarni,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tatus: preliminary; translated from GB/EMBL/DDBJ
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Similarity 38.6%;
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C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
R; Date: 282, 2012-2018, 1998
A; Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A; Reference number: A7500; MUID: 99069613; PMID: 9851916
A; Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A; Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A; Molecule type: DNA
A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-1638 <STO>
A; Coss - references: UNIPROT: 061528; UNIPARC: UPI000002A2IC; GB: chr_I; PIDN: AAC71109.1; PI
A; Odenetics:
A; Map position: 1
A; Map position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malayi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   971; NID:9156056;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brugia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              433/3; 481/3
                                                                                                                                                                                                                                                                                                                                                                              09-Jul-2004
                                                                                                                : | : | : | : DMLDKGEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 RTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQ-WQH-KQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                         63K antigen - nematode (Brugia malayi)
C;Species: Brugia malayi
C;Species: Brugia malayi
C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2
C;Accession: A54510
R;Perrine, K.G.; Denker, J.A.; Nilsen, T.W.
Mol. Biochem. Parasitol. 30, 97-104, 1988
A;Title: A multi-copy gene encodes a potentially protective antigen in E
A;Reference number: A54510; MUID:88288341; PMID:2840577
A;Accession: A54510
A;Accession: A54510
A;Accession: A54510
A;Cross-references: UNIPROT:P10723; UNIPARC:UP100001365DE; GB:J03971; NI
C;Genetics:
A;Introns: 23/2; 79/3; 140/1; 163/3; 214/1; 276/3; 321/3; 379/3; 433/3;
C;Superfamily: lysine-tRNA ligase
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                                                                                          YPGELGKRI-YNEISKEAWAQWQHKQTMLINEKKLNMMNAEHRKLLEQEMV
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                                              Indels
                                                                                                             350 YSPDNGKRVDVDKLTKEEVASWKTGDVLLLNGKILTGRDAAHKRL-
     Length
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73
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  Score 78; DB;
Pred. No. 4.8;
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Pred. No. 30;
9; Mismatches
                                              Mismatches
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                                             18;
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Similarity 30.7%;
27; Conservative 16
th Similarity 30.2%; 19; Conservative 18
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38.6%;
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Best Local S
Matches 27
  Query Match
Best Local S
Matches 19
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404/3

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228/2; 322/2;
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125/3; 191/3;
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A:Molecule type: DNA
A;Residues: 1-507 <STO>
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A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Genetics:
A;Gene: MYPU 4970
A;Genetic code: SGC3
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A,Gene: PA4333
C,Superfamily: i
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Best Local
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A; Introns:
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Best Loc
Matches
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                                                 PIDN: BAB75301
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                                                                                                                                                                                                                   16 GODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNAEHRKL-LEQEMVNFL
                                                                                                                                                                                                                                       8 TFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLI---NEKKLNMMNAEHRKL
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                                                 00019;
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C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Ju
C; Accession: T46013
R; Benes, V.; Wurmbach, E.; Drzonek, H.; Ancorgo, W.; Mewes, H.W.; Lem
submitted to the Protein Sequence Database, January 2000
A; Reference number: Z23019
A; Accession: T46013
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-265 < BEN>
A; Residues: 1-265 < BEN>
A; Experimental source: cultivar Columbia; BAC clone T10K17
A; Experimental source: cultivar Columbia; BAC clone T10K17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein KO2F3.6 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Se
C;Accession: T16527
R;Bentley, D.
Submitted to the EMBL Data Library, May 1994
A;Description: The sequence of C. elegans cosmid KO2F3.
A;Reference number: Z18530
A;Accession: T16527
A;Accession: T16527
A;Accession: T16527
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-447 <BEN>
A;Residues: 1-447 <BEN>
A;Experimental source: strain Bristol N2
C;Genetics:
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                                                   GB:BA0
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                                                                                                                                                   Length 683;
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             A;Molecule type: DNA
A;Residues: 1-683 <KUR>
A;Cross-references: UNIPROT:Q8YR48; UNIPARC:UPI00000CE850; GB:B
A;Experimental source: strain PCC 7120
C;Genetics:
A;Gene: alr3602
C;Superfamily: Synechocystis long-chain-fatty-acid-CoA ligase;
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                                                                                                                                                s Score 74.5; DE Fred. No. 14; 21; Mismatches
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622 FR-QELNREVQNRPGYRPDDR 641
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                                                                                                                                                Query Match
Best Local Similarity 28.4%;
Matches 23; Conservative 2
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A; Map position: 3
A; Introns: 42/3; 224/3; 246/3
A; Note: T10K17.120
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preliminary
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T16527
A;Status:
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M.J.; Br
K.; Lim,
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A.; Larbig,
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                           16;
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                                                                                                                                                                                                                                                                         Mizoguchi, S.D.; Warrener, c, S.N.; Folger, K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                Nature 406, 959-964, 2000
A; Title: Complete genome sequence of Pseudomonas aeruginosa PA01,
A; Reference number: A82950; MUID: 20437337; PMID: 10984043
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  Length 447;
                                                                       ---SWSQFRKSWYMFFYQNEKIPEMLCSADDMKMLE
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                                                         PGELGKRIYNEISKEAWAQWQHKQTMLI--NEKKLNMM-NAEHRKLL
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                                                                                                                                                                                                              probable fumarase randinosa
C;Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ferris, S.; Barbe, V.; -2153, 2001
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Pred. No. 18;
8; Mismatches
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Mismatches
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18;
DB
5;
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Pred. No.
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Coulter,
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C; Date: 24-May-2001 #sequence_revision 24-M
C; Accession: A99574
R; Chambaud, I.; Heilig, R.; Ferris, S.; Bar
Nucleic Acids Res. 29, 2145-2153, 2001
A; Title: The complete genome sequence of th
A; Reference number: A99512; MUID:21267165;
                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: UNIPARC: UPI00000C5CC5; A; Experimental source: strain PAO1
Score Pred.
                           11;
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illarity 28.9%;
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Similarity 25.6%;
20; Conservative 1
Query Match
Best Local Similarity 32.9%;
Matches 24; Conservative
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Radune, D.; Holtzapple
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pneumoniae.
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                                                                                                                                                                                                                                                                                                        3.; DeHoff, E
P.; McAhren,
                                                                                                                                                                                          Apy 1991

C; Species: Streptococcus pneumoniae

C; Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C; Accession: Apy 1991

R; Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszczak, L.; Burgett, S.; DeHoff, e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhri, Y. P.; Sun, P.M.; Winkler, M.E.

J. Bacteriol. 183, 5709-5717, 2001

A; Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskun; A; Reference number: A97872; MUID:21429245; PMID:11544234

A; Reference number: A97872; MUID:21429245; PMID:11544234

A; Residues: 1-258 «KUR»

A; Residues: 1-258 «KUR»

A; Residues: 1-258 «KUR»

A; Cross-references: UNIPROT:097020; UNIPROT:08CYTZ; UNIPARC:UPI000004A8FC; GB:Al

C; Genetics:

A; Genetics:

A; Genetics:

A; Genetics:
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....avision 03-Aug-2001 #text_change 09-Jul-2004
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; I nson, T.; Hickey, B.K.; Holt, I.B.
Science 293, 498-506, 2001
A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneu A;Accession: B95121
A;Accession: B95121
A;Accession: B95121
A;Residues: 1-258 «KUR»
A;Residues: 1-258 «KUR»
A;Experimental source: strain TIGR4
C;Genetics:
A;Gene: SP105.
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                      86 QDSSLYENISVYKNIYLSI-KNSWS-WKIKELSIFFEKYISDYNVKNKKIL
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Matches 18; Conservative
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                                                                                                                                                                            Denker,
                                                                                                            C; Species: Brugia malayi
C; Species: Brugia malayi
C; Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09
C; Accession: A28209
R; Nilsen, T.W.; Maroney, P.A.; Goodwin, R.G.; Perrine, K.G.; Denke Proc. Natl. Acad. Sci. U.S.A. 85, 3604-3607, 1988
A; Title: Cloning and characterization of a potentially protective A; Reference number: A28209; MUID:88217950; PMID:3368467
A; Accession: A28209
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-548 <NIL>
A; Cross-references: UNIPROT:P10723; UNIPARC:UP1000016B881; EMBL:J0
C; Superfamily: lysine-tRNA ligase
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A;Reference number: Z18416
A;Accession: T15842
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1119 <DUZ>
A;Residues: 1-1119 <DUZ>
A;Cross-references: UNIPROT:Q18859; UNIPARC:UPI0000179EE3;
C;Genetics:
A;Gene: CESP:C54G7.4
A;Introns: 6/3; 70/1; 111/2; 160/3; 180/1; 277/1; 325/3; 36
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C;Date: 20-Sep-1999 #sequence_r
C;Accession: T15842
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09-Jul-2004

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Search time 215 Seconds (without alignments) 207.113 Million cell updates/sec 91 US-09-955-502A-11 486 1 MSRTIFCTFLQREAEGQDFQ......NFLFEGKEVHIEGYTPEDKK score: Sequence: Title: Perfect

0.5 BLOSUM62 Gapop 10.0 , Gapext Scoring table:

2782304 seqs, 489333398 residues Searched:

2782304 Total number of hits satisfying chosen parameters:

2000000000 length: length: seq seq DB DB Minimum Maximum

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

A Geneseq 200701:\*

1: geneseqp1980s:\*

2: geneseqp2000s:\*

4: geneseqp2001s:\*

5: geneseqp2002s:\*

7: geneseqp2003as:\*

7: geneseqp2003as:\*

8: geneseqp2004s:\* geneseqp2006s:\* geneseqp2007s:\* Database

printed, Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being prand is derived by analysis of the total score distribution.

SUMMARIES

		78158 Am	78157 Amino ac	78156 Amino a	8161 Amino ac	81	78162 Amino ac	163 Amino a	8160 Amino ac	5445 Klebsiel	3450 Enterop	3155	165 Amino ac	164 Amino ac	Bacteria	150	3152 Amino ac	151	ጠ	78154	8166 Amino ac	78148 Amino a	7 Amino ac
ģ		815	15	B7815	16	781	7816	φ	918	44	AEH6	7815	7816	16	$\circ$	7815	ABB78152 .	ABB78151	ABB78153	ABB78154		ABB78148	ABB78147
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### ALIGNMENTS

Amino acid sequence of a YggX homologue. RESULT 1 ABB78158 ID ABB78158 standard; protein; 91 AA (first entry) 05-NOV-2002 ABB78158; X S X X X X X

Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.

Unidentified.

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hydroxyl radical; I
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Pred. No. 3.2e-46;
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Score 469; DB 5;
Pred. No. 3.2e-46;
Mismatches
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hydroxyl radical; DNA damage; YggX homologue.
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ilarity 94.5%;
Conservative
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96.5%;
94.5%;
                                                                                                                                                                                              ABB78159 standard; protein;
                                                                                                                                                                                                                                                    entry)
                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOWNS D.
GRALNICK J A
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                                                                                                                                                                                                                                                                            sequence
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           l Similarity
86; Conserv
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Best Local Similarity
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                                                                                                                                                                                                                                                    05-NOV-2002
                                                                                                                                                                                                                                                                             acid
Query Match
Best Local S
Matches 86
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(GRAL/)
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ABB7815
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**ABB78162** RESULT

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The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       le damage; cell; YggX; Salmonella enterica serovar typhimurium; radical; DNA damage; YggX homologue.
                                  Salmonella enterica serovar typhimurium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNNMNNA
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                                                                                                                                                                                                                                                                                                                                                          Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
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                                cell; YggX; Salmonella en DNA damage; YggX homologue
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                               16pp; English
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ilarity 92.3%;
Conservative
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                                                                                 Salmonella typhimurium
  of
                                                                                                                                                                                                                                                                                             Gralnick JA;
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                                 de damage;
radical; D
                                                                                                                                                                                                                                                                                                                              WPI; 2002-589476/63
                                                                                                                                                                                                                                              DOWNS D.
GRALNICK J
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                               Fig 1A;
                                                                                                                  US2002072118-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91 AA;
                                                                                                                                                                              18-SEP-2001;
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  acid
                                  Superoxide
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                                                hydroxyl
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(GRAL/)
                                                                                                                                                                                                                                                                                                DOWTHE
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ABB7816
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more than the
almonella
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oxidation
                                                                                                                                                                                                                typhimurium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cells are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes a method for reducing superoxide da cell. The method comprises engineering the cell to produce more native amount of YggX protein (a protein identified from Salmon enterica serovar typhimurium) or its homolog, where the cells a rendered more resistant to superoxide damage. YggX reduces the of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions frolusters. The resulting decrease in free-iron levels generates hydroxyl radicals and thus reduced DNA damage. The method is us reducing superoxide damage in a bacterial, yeast, mammalian or cell. ABB78147-78 represent YggX homologues
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Pred. No. 3.2e-46;
                                                                                                                                                                                                              le damage; cell; YggX; Salmonella ent
radical; DNA damage; YggX homologue
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61 EHRKLLEQEMVSFLFEGKDVHIEGYTPEDKK
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nilarity 94.5%;
Conservative
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                                                                               ABB78162 standard; protein;
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                                                                                                                                                                                Amino acid sequence
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Best Local Similarity
                                                                                                                                                                                                                                                               Salmonella typhi.
                                                                                                                                                                                                                                                                                               US2002072118-A1
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                                                                                                                                                                                                                                                                                                                                                             18-SEP-2001;
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Best Local
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                                                                                                                                                                                                 The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
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                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                              Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant expression vector; transcription regulatory element; Klebsiella pneumoniae protein; antibacterial; Vaccine.
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                                                                                                                             bacterial,
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                                                                                                                                                                                                                                                                                                                                                        Score 453; DB 5;
Pred. No. 2.2e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Klebsiella pneumoniae polypeptide segid 11962.
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                                                                                                                                                                            English.
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                                                                                                                                                                                                                                                                                                                                                       93.2%;
nilarity 94.3%;
Conservative
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                         22-SEP-2000; 2000US-0234588P
  2001US-00955502
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                                                                                                                                                                               1A; 16pp;
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                                                                                   Gralnick JA;
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                                                DOWNS D.
GRALNICK J A.
                                                                                                         WPI; 2002-589476/63.
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N-PSDB; ACH98996.
                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 83; Conser
                                                                                                                                                                                                                                                                                                                                   Sequence 88 AA;
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 18-SEP-2001;
                                                                                                                                                                               Example; Fig
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(GRAL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                             Klebsiella
                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                       76
                                                                      pneumoniae polypeptide. Also described are: a recombinant expression vector comprising the nucleic acid, operably linked to a transcription regulatory element; and a cell comprising the recombinant expression vector. The nucleic acid is useful for preparing a vaccine composition against Klebsiella pneumoniae. This is the amino acid sequence of a Klebsiella pneumoniae of the invention
                                                                                                                                                                                                                                                                                                        1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                         17 MSRTIFCTFLOREADGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLSMMNP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding an Enterobacter cloacae polypeptide, useful ting, and treating pathological conditions resulting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bacterial infection; enterobacter infection;
acid encoding a Klebsiella pneumoniae polypeptide, vaccine composition against Klebsiella pneumoniae.
                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                          Length 107;
                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                              .. m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sednence
                                                                                                                                                                                                                                          Score 450; DB 7;
Pred. No. 6.3e-44
                                                                                                                                                                                                                                                                                                                                                                                                        107
                                              932pp; English
                                                                                                                                                                                                                                                                                                                                                                         91
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165pp; English
                                                                                                                                                                                                                                                                                                                                                                                        EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      126 AA
                                                                                                                                                                                                                                                           Pred.
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                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cloacae protein
                                             NO 11962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0074787P
98US-0094145P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ບ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9887;
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                                                                                                                                                                                                                                       92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detecting, preventing, and from bacterial infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Deloughery
                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibacterial; screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2006-349670/36
                                                H
                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2006-34967U,
N-PSDB; AEH56055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid
                                                                                                                                                                                                            Sequence 107 AA;
                                                 SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Weinstock KG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Enterobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US7041814-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-FEB-1998;
24-JUL-1998;
                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUL-2006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-MAY-2006
                                                                                                                                                                                                                                                                          83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis;
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EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK
                                                                                                                     05-NOV-2002
                                                                                                                                       acid
                                                                                                 ABB78165;
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(GRAL/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plant
a
                                                                                                                                                                                                                                                                    ; cell; YggX; Salmonella enterica serovar typhimurium; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              damage to
                                                                              1 MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAOWOHKOTMLINEKKLNNMNA
                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            specification describes a method for reducing superoxide
                                        Length 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 90;
                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 , DB 5; л.
1.8e-38;
8;
                                                             4.
..
                                       ; DB 10;
3.2e-42;
                                       ed. No. 3.2e
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 402; DB Pred. No. 1.8e 7; Mismatches
                                                                                                                     61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK 90
                                                                                                                               a YggX homologue
                                       Score
Pred.
                                                          .
9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         English.
                                      89.7%;
nilarity 88.9%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                           2001US-00955502
                                                                                                                                                                                                                                                                                                                                                                              2000US-0234588P
                                                                                                                                                                                       ABB78155 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         82.7%;
larity 83.3%;
Conservative
                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                Amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1A; 16pp;
                                                                                                                                                                                                                                                                                                                                                                                                                             Gralnick JA;
                                                                                                                                                                                                                                                                                                                                                                                                 (DOWN/) DOWNS D.
(GRAL/) GRALNICK J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-589476/63.
                                                                                                                                                                                                                                                                    de damage;
radical; D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 75; Conser
                                       Query Match
Best Local Similarity
                      Sequence 126 AA;
                                                                                                                                                                                                                                                                                                 Vibrio cholerae
                                                                                                                                                                                                                                                                                                                   US2002072118-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 90 AA;
                                                                                                                                                                                                                                                                                                                                                                             22-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Fig
                                                                                                                                                                                                                                                                                                                                                         18-SEP-2001;
                                                                                                                                                                                                                                                                                                                                       13-JUN-2002
                                                                                                                                                                                                                              05-NOV-2002
                                                         80;
                                                                                                                                                                                                                                                                     Superoxide
                                                                                                                                                                                                          ABB78155;
                                                                                                                                                                                                                                                                              hydroxyl
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                                                           Matches
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ABB7815
SXS
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The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                      Salmonella enterica serovar typhimurium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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Pred. No. 9.1e-38;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                      Superoxide damage; cell; YggX; Salmonella ent
hydroxyl radical; DNA damage; YggX homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90
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                                                                                                                                                                                                                                                                                                      a YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           81.5%;
llarity 82.2%;
Conservative 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-SEP-2000; 2000US-023458BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-SEP-2001; 2001US-00955502
                                                                                                                                                ABB78165 standard; protein;
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GRALNICK J A.
                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                       sednence
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Best Local Similarity
Matches 74; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fig 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US2002072118-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Unidentified.
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1 MARTVFCTRLQKEADGLDFQLYPGELGKRIFDNICKEAWAQWQTKQTMLINEKKLNMMDP 60

В

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MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAOWOHKOTMLINEKKLNMMNA

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(DOWN/) DOWNS
                                                                    (GENO-)
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Matches
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EXEXE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mirabilis infection; bacterial infection; antibacter
                                                Superoxide damage; cell; YggX; Salmonella enterica serovar
hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           7
                                                                                                                                                                                                                                                                                                                                                                                                                                        5,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 395; DB 5
Pred. No. 1e-37;
2; Mismatches
                              Amino acid sequence of a YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93 AA
                                                                                                                                                                                                                                                                                        Example; Fig 1A; 16pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     78
                                                                                                                                                                                                                                                                                                                                                                                                                                       81.3%;
ilarity 94.9%;
Conservative ;
                                                                                                                                        2001US-00955502
                                                                                                                                                           2000US-0234588P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADF05158 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EHRKLLEQEMVNFLFEGK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
           (first entry)
                                                                                                                                                                                                           Gralnick JA;
                                                                              Klebsiella pneumoniae
                                                                                                                                                                              DOWNS D.
GRALNICK J A.
                                                                                                                                                                                                                              2002-589476/63
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 74; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mirabilis.
                                                                                                  US2002072118-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 78 AA;
                                                                                                                                       18-SEP-2001;
                                                                                                                                                          22-SEP-2000;
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           05-NOV-2002
                                                                                                                      13-JUN-2002
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Best Local S
Matches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADF05158;
                                                                                                                                                                                                         Downs D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                              (DOWN/)
(GRAL/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proteus
                                                                                                                                                                                                                             WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADF051
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The invention relates to new Proteus mirabilis polypeptides and... polypucleotides. The invention also relates to antibodies against the polypeptides, a method of generating vaccines for immunising an individual against P. mirabilis, a method for evaluating a compound for the ability to bind a P. mirabilis polypeptide and a method for screening test compounds for anti-bacterial activity. The polypeptides and polynucleotides are useful as molecular targets for diagnosing, preventing and treating pathological conditions resulting from bacterial infection, as reagents for diagnosis of bacterial diseases, as components of antibacterial vaccines, as targets for antibacterial drugs or as bio-control agents for plants. This sequence represents a Proteus mirabilis polypeptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  enterica serovar typhimurium;
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0
                                                                                                                                                                                                                                                                                                        New Proteus mirabilis polypeptides and polynucleotides, useful reagents for diagnosis of bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 93;
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Pred. No. 6.1e-37
7; Mismatches 1.
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YggX homologue
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radical; DNA damage;
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                                             2000US-00543681
                                                                                            99US-0128706P
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larity 80.0%;
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N-PSDB; ADF00986.
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                                             05-APR-2000;
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12-AUG-2003
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                                                        Reducing superoxide damage to a cell, e.g. bacterial, mammal cell, comprises engineering the cell to produce more YggX pr
protein identified from Salmonella enterica Serovar Typhimur
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Pred. No. 7.8e-37
11; Mismatches 1
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YggX homologue.
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                                                                                              1A; 16pp; English
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ilarity 76.9%;
Conservative 1
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GRALNICK J
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nes 70; Conser
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GRALNICK
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cell. The method comprises a method for reducing superoxide damage to a native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homoloques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell; YggX; Salmonella enterica serovar typhimurium; DNA damage; YggX homologue.
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Pred. No. 9.6e-37
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GRALNICK J A.
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hydroxyl radical; I
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                                               Length 87;
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                                             Score 379; DB 5;
Pred. No. 8.1e-36
1; Mismatches
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                                                                                                                                                                                                                                                                                           standard; protein; 87
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                                             78.0%;
larity 75.9%;
Conservative 1
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              Sequence 87 AA;
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                                                                                                                                                                                                                                                                                                                          ABB78153;
                                                                                                                                                                                                                                                                                         ABB78153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (DOWN/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                              Matches
                                                                                                                                                                                                                                                          RESULT 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mammalian or
YggX protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Typhimurium
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    e.g. bacterial,
    to produce more
enterica Serovar 1

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16;
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Pred. No. 2.3e-30,
2; Mismatches 16
                                                                                                                                                                                                                                                                                     ; cell; YggX; Salmonella ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
                                                                                                                                                                                                                                                   a YggX homologue
                                      87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reducing superoxide damage to a cell, cell, comprises engineering the cell to protein identified from Salmonella ent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDRKFLEAQMTSFLFEGKDVEIEGFVPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-SEP-2001; 2001US-00955502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-SEP-2000; 2000US-0234588P
                                                                                                                                   standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABB78166 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gralnick JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ď
                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                   Amino acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-589476/63
                                                                                                                                                                                                                                                                                       de damage;
radical; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GRAL/) GRALNICK
                                                                                                                                                                                                                                                                                                                                                                                     US2002072118-A1
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                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                              05-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-2002
                                                                                                                                                                                                                                                                                        Superoxide
                                                                                                                                                                         ABB78154;
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Best Local S
Matches 60
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                                                                                                                                   ABB78154
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                                                                                                                                                                                                                                                                                                             hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 20
ABB78166
                                                                                               RESULT 19
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The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          enterica serovar typhimurium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MSRIVNCVKLKREAEGLDFPPYPGELGTRIWQQISKEAWEEWKQIQTRLVNENRLNLADA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 255; DB 5;
Pred. No. 1.9e-21,
; Mismatches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Salmonella ent
YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a YggX homologue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 EHRKLLEQEMVNFLFEGKEVHIEGYTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RARKYLOQOMERFLFEDGTVEAQGYVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          le damage; cell; YggX;
radical; DNA damage;
                                                                                                                                                                                                                                                                                  16pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001US-00955502.
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                                                                  2000US-0234588P
                                 18-SEP-2001; 2001US-00955502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.5%;
55.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB78147 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of
                                                                                                                                                  Gralnick JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gralnick JA;
                                                                                                  DOWNS D.
GRALNICK J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bordetella pertussis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
                                                                                                                                                                                  WPI; 2002-589476/63
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Best Local Similarity
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GRALNICK
                                                                                                                                                                                                                                                                                   Fig 1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2002072118-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 87 AA;
                                                               22-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-JUN-2002.
13-JUN-2002
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                                                                                                                                                                                                                                                                                     Example;
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(GRAL/)
                                                                                                  (DOWN/)
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                                                                                                                                                    DOWING
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<del>Q</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       more than the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                       plant
                                                                   yphimurium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yphimurium;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       specification describes a method for reducing superoxide
                                                                  serovar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                   enterica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Salmonella enterica
YggX homologue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 265; DB 5;
Pred. No. 1.1e-22
                                                                                 YggX homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                  Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence of a YggX homologue.
                                   a YggX homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               87 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ie damage; cell; YggX;
radical; DNA damage; '
                                                                 le damage; cell; YggX;
radical; DNA damage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 1A; 16pp; English
                                                                                                                                                                                                                                                    2000US-0234588P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          54.5%;
61.8%;
                                                                                                                                                                                                                    2001US-00955502
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EHRKLLEQEMVNFLFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bordetella parapertussis
                                   of
                                                                                                                                                                                                                                                                                                                                     JA;
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                                 sednence
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                                                                                                                                                                                                                                                                                    DOWNS D. GRALNICK J
                                                                                                                                                                                                                                                                                                                                     Gralnick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB78148 standard;
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                                                                                                                                                  US2002072118-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 76 AA;
                                                                                                                                                                                                                                                    22-SEP-2000;
                                                                                                                  Unidentified
                                                                                                                                                                                                                    18-SEP-2001;
05-NOV-2002
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                                 Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid
                                                                 Superoxide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superoxide
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                                                                                     hydroxyl
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Best Local
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RESULT 21 **ABB78148** 

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Gaps

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Indels

26;

Length 87;

YggX reduces the oxidation of Fe(II) ions from levels generates fewer The method is useful for

mammalian

cells are

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serovar typhimurium) or its homolog, more resistant to superoxide damage. Clusters, and thus reduces the loss. The resulting decrease in free-iron

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of (Fe-S)
                                 clusters.
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                                                                                     cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from Salmonella enterica serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues
                                                                                                                                                                                                                                                                           9
                       plant
a
                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.
                                                                                                                                                                                                                                                                           EKKLNIMINA
                                                                                                                                                                                                                                                                                      Gaps
                    Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.
                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                            1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLIN
                                                                                                                                                                                                                                 Length 87;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                    ; DB S; Le
1.9e-21;
26;
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                Score 255;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                       87
                                                                                                                                                                                                                                                                                                                                            87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of a YggX homologue
                                                                                                                                                                                                                                                                                                                                          61 RARKYLQQQMERFLFEDGTVEAQGYVP
                                                                                                                                                                                                                                                                                                                       EHRKLLEQEMVNFLFEGKEVHIEGYTP
                                                                                                                                                                                                                                                                                                                                                                                                   Z
                                                                                                                                                                                                                                                      13;
                                                                 English
                                                                                                                                                                                                                                                                                                                                                                                                  ABB78149 standard; protein; 86
                                                                                                                                                                                                                              52.5%; Edilarity 55.2%; Edonservative 13;
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Vandenesch F;
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A, Kunst
hydroxyl radicals and thus reduced DNA damage. The reducing superoxide damage in a bacterial, yeast, cell. ABB78147-78 represent YggX homologues
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25;
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Pred. No. 7.7e-20
3; Mismatches 21
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Magnier
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54.8%;
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Reducing superoxide damage to a cell, e.g. bacterial, mammalian or cell, comprises engineering the cell to produce more YggX protein, protein identified from Salmonella enterica Serovar Typhimurium.

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The specification describes a method for reducing superoxide cell. The method comprises engineering the cell to produce monative amount of YggX protein (a protein identified from Salm

English.

Example; Fig 1A; 16pp;

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Deneumophila. The present squence represents the amino acid sequence of a L. pneumophila protein.
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                                                                     47.6%; Score 231.5; DB larity 53.8%; Pred. No. 1e-18; Conservative 17; Mismatches
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Zidane N, Magnier
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Rusniok C, Bouchier C,
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protein search, using sw model OM protein

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US-09-955-502A-11 486 1 MSRTIFCTFLQREAEGQDFQ......NFLFEGKEVHIEGYTPEDKK Title: Perfect score: Sequence:

0.5 BLOSUM62 Gapop 10.0 , Gapext

Scoring table:

3281787 seqs, 1072124677 residues Searched:

3281787 Total number of hits satisfying chosen parameters

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Database

UniProt\_8.4:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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### ALIGNMENTS

NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
PubMed=16275786; DOI=10.1093/nar/gki954;
Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X., Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S., Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y., Qiang B., Hou Y., Yu J., Jin Q.;
"Genome dynamics and diversity of Shigella species, the etiologic agents of bacillary dysentery.";
Nucleic Acids Res. 33:6445-6458(2005). 11-JUL-2006, integrated into UniProtKB/Swiss-Prot.
06-DEC-2005, sequence version 1.
11-JUL-2006, entry version 7.
Probable Fe(2+)-trafficking protein.
Name=yggX; OrderedLocusNames=SBO\_3028;
Shigella boydii serotype 4 (strain Sb227).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBI\_TaxID=300268; 91 AA. PRT; STANDARD; PETP SHIBS SHIBS RESULT FETP 

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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     agents of bacillary dysentery.";

Nucleic Acids Res. 33:6445-6458(2005).

-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).

-!- SUBUNIT: Monomer (By similarity).
   and/or
                                                                                                                                                                                                                                                                                                                     1 MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                                                                                                                                   1 MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
  synthesis and
y similarity)
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PubMed=16275786; DOI=10.1093/nar/gki954;
Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,
Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.
Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,
Qiang B., Hou Y., Yu J., Jin Q.;
"Genome dynamics and diversity of Shigella species, the etiologic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ales;
 acquisition and iron-requiring processes, such as synthesis repair of Fe-S clusters in biosynthetic enzymes (By similarit SUBUNIT: Monomer (By similarity).
SIMILARITY: Belongs to the Fe(2+)-trafficking protein family
                                                                                                                                                                                                                  Probable Fe(2+)-trafficking protein
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11-JUL-2006, entry version 7.
Probable Fe(2+)-trafficking protein.
Name=yggX; OrderedLocusNames=SDY 3110;
Shigella dysenteriae serotype 1 (strain Sd197).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteria
Enterobacteriaceae; Shigella.
NCBI TaxID=300267;
                                                                                                                                                                                                                                                                       91;
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                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                            CRC64;
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1E3625B77C32B94B CR0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     032C31;
11-JUL-2006, integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                   Score 486; DB 1;
Pred. No. 7.3e-42;
); Mismatches 0;
                                                                                          CP000036; ABB67534.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                        91
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                                                                                                                                                                                                                                                                                                                                                                      HAMAP; MF_00686; -; 1. _____InterPro; IPR007457; YggX.
Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe_traffic_YggX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CP000034_GR; SDY_3110
                                                                                                                             CP000036_GR; SBO_3028
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ilarity 100.0%;
Conservative 0
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Matches 91
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity). SUBUNIT: Monomer (By similarity). SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                  1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
                                                                                                                                                                                                                             1 MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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PubMed=16275786; DOI=10.1093/nar/gki954;

Yang F., Yang J., Zhang X., Chen L., Jiang Y., Yan Y., Tang X.,

Wang J., Xiong Z., Dong J., Xue Y., Zhu Y., Xu X., Sun L., Chen S.,

Nie H., Peng J., Xu J., Wang Y., Yuan Z., Wen Y., Yao Z., Shen Y.,

Qiang B., Hou Y., Yu J., Jin Q.;

"Genome dynamics and diversity of Shigella species, the etiologic

agents of bacillary dysentery.";

Nucleic Acids Res. 33:6445-6458(2005).

-!- FUNCTION: Could be a mediator in iron transactions between iron
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Shigella.
NCBI_TaxID=300269;
                                  Probable Fe(2+)-trafficking protein/
FTId=PRO 0000246117.
1E3625B77C32B94B CRC64;
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/FTId=PRO 0000246118.
1E3625B77C32B94B CRC64;
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                                                                                                                  486; DB 1;
No. 7.3e-42;
matches 0;
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Pred. No. 7.3e-42
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Pred.
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DUF495;
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License
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Escherichia coli O157:H7.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=0157:H7 / EDL933 / ATCC 700927 / EHEC;
MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D
                                                                                                                                                                                                                         PubMed=16585510; DOI=10.1073/pnas.0600938103;
Chen S.L., Hung C.-S., Xu J., Reigstad C.S., Magrini V., Sabalasiar D., Bieri T., Meyer R.R., Ozersky P., Armstrong J.R. Fulton R.S., Latreille J.P., Spieth J., Hooton T.M., Mardis Hultgren S.J., Gordon J.I.;
"Identification of genes subject to positive selection in uropathogenic strains of Escherichia coli: A comparative generative generation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1E3625B77C32B94B CRC64;
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POA8P4; P52065;
O7-JUN-2005, integrated into UniProtKB/Swiss-Prot.
O7-JUN-2005, sequence version 1.
11-JUL-2006, entry version 11.
Probable Fe(2+)-trafficking protein.
Name=yggX; OrderedLocusNames=Z4307, EC83838;
Escherichia coli O157:H7.
                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 103:5977-5982 (2006)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 486; DB 2;
Pred. No. 7.3e-42;
); Mismatches 0;
                                                                                         Uni ProtKB/TrEMBL
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61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK
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InterPro; IPR007457; YggX.
Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
                                                                                       16-MAY-2006, integrated into UniProtKB
16-MAY-2006, sequence version 1.
11-JUL-2006, entry version 4.
Hypothetical protein yggX.
Name=yggX; ORFNames=UTI89 C3353;
Escherichia coli (strain UTI89 / UPEC)
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Enterobacteriaceae; Escherichia
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                                                                                                                                                                                                      SEQUENCE.
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                                                                                                                                                                                TaxID=364106;
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STRAIN=UT189
                                                                 QIR763_ECOUT
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STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC;

MEDLINE=21156231; PubMed=11258796; DOI=10.1093/dnares/8.1.11;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,

Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli
"Complete genomic comparison with a laboratory strain K-12.";

O157:H7 and genomic comparison with a laboratory strain K-12.";

DNA Res. 8:11-22(2001).

-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).
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Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A. Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L., Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C., Welch R.A., Blattner F.R.; "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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Probable Fe(2+)-trafficking
/FTId=PRO_0000214479.
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to the Fe(2+)-trafficking
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POA8P3; P52065; Q2M9N1;
07-JUN-2005, integrated into UniProtKB/Swiss-Prot 07-JUN-2005, sequence version 1.
11-JUL-2006, entry version 12.
Probable Fe(2+)-trafficking protein.
Name=yggX; OrderedLocusNames=b2962;
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NO. 2.3e-41;
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Escherichia coli.
Bacteria; Proteobacteria; Gammaproteobacteria;
Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
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NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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EMBL; BA000007; BAB37261.1;
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GenomeReviews; AE005174_GR;
                                                                                                                                     Nature 409:529-533(2001).
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F91108; F91108
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land V.,
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rotein YggX
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o
                                                                                                                       NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=K12 / W3110 / ATCC 27325 / DSM 5911;
DOI=10.1038/msb4100049;
Hayashi K., Morooka N., Yamamoto Y., Fujita K., Isono K., Choi S., Ohtsubo E., Baba T., Wanner B.L., Mori H., Horiuchi T.;
"Highly accurate genome sequences of Escherichia coli K-12 strains MG1655 and W3110.";
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                                                  G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INDUCTION: By oxidative stress and soxS. SIMILARITY: Belongs to the Fe(2+)-trafficking protein family
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                                                                                                                                                                                                                                                                    PARTIAL PROTEIN SEQUENCE OF 1-12.

STRAIN=K12 / EMG2;

MEDLINE=97443975; PubMed=9298646;

Link A.J., Robison K., Church G.M.;

"Comparing the predicted and observed properties of proteins in the genome of Escherichia coli K-12.";

Electrophoresis 18:1259-1313(1997).
STRAIN=K12 / MG1655 / ATCC 47076;
MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.53
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burl Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D Mau B., Shao Y.;
"The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;
Pomposiello P.J., Koutsolioutsou A., Carrasco D., Demple B.;
"SoxRS-regulated expression and genetic analysis of the yggX
Escherichia coli.";
J. Bacteriol. 185:6624-6632(2003).
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PubMed=15883188; DOI=10.1110/ps.051358105;
Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gel Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gel The solution structure of the oxidative stress-related prot from Escherichia coli.";
Protein Sci. 14:1673-1678(2005).
-!- FUNCTION: Could be a mediator in iron transactions between acquisition and iron-requiring processes, such as synthem repair of Fe-S clusters in biosynthetic enzymes. Necessa: maintain high levels of aconitase under oxidative stress maintain high levels of aconitase under oxidative stress
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99420866; PubMed=10493123;
DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELPS218
Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs
"Enrichment of low abundance proteins of Escherichia coli by hydroxyapatite chromatography.";
Electrophoresis 20:2181-2195(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.unipro
Distributed under the Creative Commons Attribution-NoDerivs
                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99085675; PubMed=9868784;
Wasinger V.C., Humphery-Smith I.;
"Small genes/gene-products in Escherichia coli K-12.";
FEMS Microbiol. Lett. 169:375-382(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U28377; AAA69129.1; -; Genomic_DNA.
EMBL; U00096; AAC75999.1; -; Genomic_DNA.
EMBL; AP009048; BAE77025.1; -; Genomic_DN
PIR; A65082; A65082.
PDB; 1YHD; NMR; A=1-90.
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SWISS-2DPAGE; POA8P3; COLI. GenomeReviews; U00096\_GR; b2962

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=ATCC 700930 / 2457T / Serotype 2a;
MEDLINE=22590274; PubMed=12704152;
DOI=10.1128/IAI.71.5.2775-2786.2003;
Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W., Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
                                                                                                                                                Probable Fe(2+)-trafficking protein /FTId=PRO_0000214478.
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                                                                                                                       sequencing;
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STRAIN=301 / Serotype 2a;

MEDLINE=22272406; PubMed=12384590; DOI=10.1093/nar/gkf566;

Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J.,

Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D
Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K.,
Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTML
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ng J., Yang G., W.
Zhu J., Kan B., Din
n., Qiang B., V
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                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria, Proteobacteria, Gammaproteobacteria,
Enterobacteriaceae, Shigella.
NCBI_TaxID=623;
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           HAMAP; MF_00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
3D-structure; Complete proteome; Director
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ilarity 100.0%;
Conservative 0
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10821 MW;
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NCBI_TaxID=591;
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11-JUL-2006,
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HAMAP; M
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MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
"Extensive mosaic structure revealed by the complete genome sequence
of uropathogenic Escherichia coli.";
Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
-!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Fe-S clusters in biosynthetic enzymes (By similarity).
                                                                             sis and/or
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 SRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNAE
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Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S., Schwartz D.C., Blattner F.R.; "Complete genome sequence and comparative genomics of Shigella flexneri serotype 2a strain 2457T."; Infect. Immun. 71:2775-2786(2003).

-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and, repair of Fe-S clusters in biosynthetic enzymes (By similarity).

-!- SUBUNIT: Monomer (By similarity).
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                                                                                                                                                                                                                                                                                                                   By similarity.
Probable Fe(2+)-trafficking protein.
/FTId=PRO 0000214507.
D7C66C2A35E62402 CRC64;
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SIMILARITY: Belongs to the Fe(2+)-trafficking protein
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25-JUL-2003, integrated into UniProtKB/Swiss-Prot.
25-JUL-2003, sequence version 2.
11-JUL-2006, entry version 21.
Probable Fe(2+)-trafficking protein.
                                                                                                                                                                                                                                                                                                                                                                           481; Db 1,
NO. 2.3e-41;
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Pred. No.
                                                                                                                                                                                                                                        Pfam; PF04362; Iron traffic; 1.
PIRSF; PIRSF029827; Fe traffic_YggX; 1.
ProDom; PD029191; DUF495; 1.
Complete proteome; Iron.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=yggX; OrderedLocusNames=c_3550;
                                                                                                                                                                                                               GenomeReviews; AE014073_GR; S_3162
GenomeReviews; AE005674_GR; SF2959
HAMAP; MF_00686; -; 1.
InterPro; IPR007457; YggX.
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Bacteria; Proteobacteria; Gamma;
Enterobacteriaceae; Escherichia
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100.0%;
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ID FETP E
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Creative Commons Attribution-NoDerivs License
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Nucleic Acids Res. 33:1690-1698(2005).

-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and repair of Fe-S clusters in biosynthetic enzymes (By similarity).

-!- SUBUNIT: Monomer (By similarity).

-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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genome sequence of Salmonella enterica serovar Choleraesuis,
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Probable Fe(2+)-trafficking protein.
/FTId=PRO 0000214502.
                                                                                                                                                                                                                                                                      By similarity.
Probable Fe(2+)-trafficking protein/FTId=PRO 0000214480.
D7C66C2A35E63692 CRC64;
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Enterobacteriaceae; Salmonella.
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                                                                Genomic DNA
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PubMed=15781495; DOI=10.1093/nar/gki297;
Tang P., Chu C., Hu S., Bao
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=yggX; OrderedLocusNames=SCH_3052;
Salmonella choleraesuis.
                                                                                                                                              HAMAP; MF_00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe_traffic_YggX;
ProDom; PD029191; DUF495; 1.
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Probable Fe(2+)-trafficking protein
                                                                                                         3550.
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BioCyc; EC0L199310:C3550-MONOMER;
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InterPro; IPR007457; YggX.
Pfam; PF04362; Iron traffic;
ProDom; PD029191; DUF495; 1.
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98.9%;
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Q8FE19; 1-90.
     the UniProt
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License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity). SUBUNIT: Monomer (By similarity). SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                             SRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKQTMLINEKKLNMMNAE
                                                                SRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAOWOHKOTMLINEKKLINMMNAE
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Layman D.,
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19-JUL-2005, sequence version 2.
11-JUL-2006, entry version 11.
Probable Fe(2+)-trafficking protein.
Name=yggx; OrderedLocusNames=SPA2974;
Salmonella paratyphi-a.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
NCBI_TaxID=54388;
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Distributed under the Creative Commons Attribution-NoDerivs 1
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Probable Fe(2+)-trafficking prot/FTId=PRO_0000214503.
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                      Length 90;
                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=ATCC 9150 / SARB42;

PubMed=15531882; DOI=10.1038/ng1470;

McClelland M., Sanderson K.E., Clifton S.W., Latreille P., Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McL Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G., Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Lay Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Spieth J., Wilson R.K.;

"Comparison of genome degradation in Paratyphi A and Typhi restricted serovars of Salmonella enterica that cause typh Nat. Genet. 36:1268-1274(2004).
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1.3e-39;
B3B6A1EE22555E3C
                               ed. No. 1.3e-39
Mismatches
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                      DB
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                     Score 464;
                                                                                                                       61 HRKLLEQEMVSFLFEGKDVHIEGYTPEDKK
                                                                                                            HRKLLEQEMVNFLFEGKEVHIEGYTPEDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 464;
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HAMAP; MF_00686; -; 1.
InterPro; IPR007457; Yggx.
Pfam; PF04362; Iron_traffic;
ProDom; PD029191; DUF495; 1.
10768 MW;
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                                94.48;
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85; Conser
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90 AA;
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Best Local
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MEDLINE=22531367; PubMed=12644504;

DOI=10.1128/JB.185.7.2330-2337.2003;

Dong W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,

Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;

"Comparative genomics of Salmonella enterica serovar Typhi strains 7 and CT18.";

J. Bacteriol. 185:2330-2337(2003).

-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and, repair of Fe-S clusters in biosynthetic enzymes (By similarity).

-!- SUBUNIT: Monomer (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
"Complete genome sequence of a multiple drug resistant Salmoneila enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Salmonella.
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Probable Fe(2+)-trafficking protein.
/FTId=PRO_0000214504.
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SIMILARITY: Belongs to the Fe(2+)-trafficking protein family
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=CT18;
MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
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                                                                                                                                                                           FETP SALTI STANDARD; PRT; 90 AA. P67618; Q8XFV6; 11-OCT-2004, integrated into UniProtKB/Swiss-Prot 11-OCT-2004, sequence version 1. 11-JUL-2006, entry version 14. Probable Fe(2+)-trafficking protein. Name=yggX; OrderedLocusNames=STY3266, t3024; Salmonella typhi.
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Pred. No. 1.3e-39;
; Mismatches 0
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61 HRKLLEQEMVSFLFEGKDVHIEGYTPEDKK
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GenomeReviews; AE014613 GR; t3024.
HAMAP; MF 00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PF04362; Iron traffic; 1.
PIRSF; PIRSF029827; Fe traffic YggX; 1.
ProDom; PD029191; DUF495; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI TaxID=601;
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SRTIFCTFLORBAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNNMNAE

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Distributed under the Creative Commons Attribution-NoDerivs License
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PubMed=15516576; DOI=10.1128/JB.186.22.7626-7634.2004;

Skovran E., Lauhon C.T., Downs D.M.;

"Lack of YggX results in chronic oxidative stress and uncovers subtle defects in Fe-S cluster metabolism in Salmonella enterica.";

J. Bacteriol. 186:7626-7634(2004).

J. Bacteriol. 186:7626-7634(2004).

-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes. Necessary to maintain high levels of aconitase under oxidative stress.

-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
  KKLINMMNAE
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                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=LT2 / SGSC1412 / ATCC 700720;
MEDLINE=21534948; PubMed=11677609; DOI=10.1038/35101614;
MCClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Laymar Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E. Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                         P67617; QBXFV6;
11-OCT-2004, integrated into UniProtKB/Swiss-Prot.
11-OCT-2004, sequence version 1.
11-JUL-2006, entry version 16.
Probable Fe(2+)-trafficking protein.
Name=yggX; OrderedLocusNames=STM3111;
Salmonella typhimurium.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriaceae; Salmonella.
NCBI TaxID=602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gralnick J.A., Downs D.M.; "Protection from superoxide damage associated with an increased of the YggX protein in Salmonella enterica."; Proc. Natl. Acad. Sci. U.S.A. 98:8030-8035(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               enterica is involved in Fe(II)
WA damage caused by hydroxyl ra
SRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKQTMLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=LT2;
PubMed=12670952; DOI=10.1074/jbc.M301577200;
Gralnick J.A., Downs D.M.;
The YggX protein of Salmonella enterica is inverseficking and minimizes the DNA damage caused residue Cys-7 is essential for YggX function.";
J. Biol. Chem. 278:20708-20715(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=LT2;
PubMed=11416172; DOI=10.1073/pnas.151243198;
                                                                                                                                              90 AA
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                                  62 HRKLLEQEMVNFLFEGKEVHIEGYTPEDKK
                                               61 HRKLLEQEMVSFLFEGKDVHIEGYTPEDKK
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StyGene; SG????; yggx.
HAMAP; MF 00686; -; 1.
InterPro; IPR007457; Yggx.
Pfam; PF04362; Iron_traffic; 1.
                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND MUTAGENESIS OF CYS-6
                                                                                                                                                                                                                                                                                                                                                                                                   Courtney L., Porwollik S., A Leonard S., Nguyen C., Scott Ryan E., Sun H., Florea L., Waterston R., Wilson R.K.; "Complete genome sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 413:852-856(2001).
                                                                                                                                              STANDARD;
                                                                                                                                               SALTY
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Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SRTI FCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAOWOHKOTMLINEKKLINMMNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=SCRI 1043 / ATCC BAA-672;

PubMed=15263089; DOI=10.1073/pnas.0402424101;

Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,

Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,

Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.

Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,

Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,

Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;

"Genome sequence of the enterobacterial phytopathogen Erwinia
carotovora subsp. atroseptica and characterization of virulence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ors.";
. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/acquisition and iron-requiring processes, such as synthesis and/
                                               By similarity.
Probable Fe(2+)-trafficking protein.
/FTId=PRO_0000214505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwinia carotovora subsp. atroseptica (Pectobacterium atroseptici
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
Enterobacteriaceae; Pectobacterium.
NCBI_TaxID=29471;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       repair of Fe-S clusters in biosynthetic enzymes (By similari SUBUNIT: Monomer (By similarity).
SIMILARITY: Belongs to the Fe(2+)-trafficking protein family
                                                                                              activity.
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                                                                                               Strong decrease
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Pred. No. 1.3e-39;
Mismatches
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    Н
  traffic_YggX;
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                                  Complete proteome;
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PIRSF; PIRSF029827; Fe to ProDom; PD029191; DUF495 3D-structure; Complete point MET 0 0 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=IP32953 / Serotype I;
PubMed=15358858; DOI=10.1073/pnas.0404012101;
Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O., Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L., Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C., Simonet M., Chenal-Francisque V., Souza B., Dacheux D., Elliott J.M., Derbise A., Hauser L.J., Garcia E.;
"Insights into the evolution of Yersinia pestis through whole-genome comparison with Yersinia pseudotuberculosis.";
"Insights into the avolution of resinia pestis through whole-genome comparison with Yersinia pseudotuberculosis.";
Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gammaproteobacteria; Enterobacteriales
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ngs to the Fe(2+)-trafficking protein family
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                                                                                                                             Probable Fe(2+)-trafficking pro/
/FTId=PRO 0000214481.
9B295D34B542D8A3 CRC64;
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C7375E7954752E64 CRC64;
                                                                                                                                                                                                                                          MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLIN
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                                                                                                                                                                         Score 411; DB 1; Le
Pred. No. 3.5e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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             DNA
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                                                                                                                                                                                                                                                                                                            DDRKLLEQEMIKFLFEGKDVHIEGYTP 87
             Genomic
                                                 HAMAP; MF 00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PF04362; Iron traffic; 1.
PIRSF; PIRSF029827; Fe traffic YggX;
ProDom; PD029191; DUF495; 1.
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PIRSF; PIRSF029827; Fe traffic YggX;
ProDom; PD029191; DUF495; 1.
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11-JUL-2006, entry version 13.
Probable Fe(2+)-trafficking protein
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Enterobacteriaceae; Yersinia
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                                                                                                                                                                                     84.6%;
                                BX950851_GR;
            CAG73886.1;
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Q666M3; 1-90.
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InterPro; IPR007457;
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76; Conserv
                                                                                                                      Complete proteome;
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             BX950851;
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                                      GenomeReviews;
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                          Q6D8J9;
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Best Local
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            EMBL;
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-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).

-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                  1 MSRTIFCTFLOREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=ATCC 39315 / El Tor Inaba N16961 / Serotype Ol;
STRAIN=ATCC 39315 / El Tor Inaba N16961 / Serotype Ol;
MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.I Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L., Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
"DNA sequence of both chromosomes of the cholera pathogen Vibrio
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/FTId=PRO 0000214508.
972331B2600B3184 CRC64;
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Vibrionaceae; Vibrio.
NCBI_TaxID=666;
Length 90;
                                           Indels
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Pred. No. 3e-33;
; Mismatches 8;
  DB 1;
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                              Mismatches
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Score 404;
Pred. No. 1
                                                                                                                                                                       61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDK
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HAMAP; MF 00686; -; 1.
InterPro; IPR007457; Yggx.
Pfam; PF04362; Iron traffic; 1.
ProDom; PD029191; DUF495; 1.
Complete proteome; Iron.
CHAIN
                                                                                                                                                                                                                                                                                                                                                                            01-OCT-2000, sequence version 1.
25-JUL-2006, entry version 23.
Probable Fe(2+)-trafficking protein.
OrderedLocusNames=VC0451;
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  83.1%;
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Best Local Similarity 83.3
----- 75; Conservative
                                           Conservative
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                      Similarity 75; Conser
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01-OCT-2000,
25-JUL-2006,
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                                                                                                                                                                                                                  iron
                                                                                                                                                                                                                                                                                                                                                                                       Probable Fe(2+)-trafficking protein. /FTId=PRO 0000214511. 7EA0CB75840A255C CRC64;
                                                                                                                                                                                          "Complete genome sequence of Vibrio vulnificus CMCP6.";
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Could be a mediator in iron transactions between in acquisition and iron-requiring processes, such as synthesis repair of Fe-S clusters in biosynthetic enzymes (By similarities).
-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
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Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su
                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprotDistributed under the Creative Commons Attribution-NoDerivs I
                                                                                                                                                            Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong
Choy H.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OrderedLocusNames=VV2885;
Vibrio vulnificus (strain YJ016).
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                     Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 90
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                                          into UniProtKB/Swiss-Prot.
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                                                                                                                                                  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
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Mismatches
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                                                                                                                                                                                                                                                                                                         01-MAR-2003, sequence version 1.
11-JUL-2006, entry version 19.
Probable Fe(2+)-trafficking protein.
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11-JUL-2006, entry version 20.
Probable Fe(2+)-trafficking protein.
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GenomeReviews; AE016795 GR; VV1 151
BioCyc; VVUL216895:VV11514-MONOMER;
                                                                                                                                                                                                                                                                                                                                  HAMAP; MF 00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PF04362; Iron traffic; 1.
ProDom; PD029191; DUF495; 1.
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                                                                                  OrderedLocusNames=VV1_1514;
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                     STANDARD;
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                                          integrated
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                                                                                                                  Vibrio
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                                                                                             Vibrio vulnificus.
                                                                                                                                                                                                                                                                                                                                                                                                              90 AA;
                                                                                                                  Vibrionaceae; V
NCBI_TaxID=672;
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                     VIBVU
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         PETP_VIBVU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

STRAIN=RIMD 2210633 / Serotype 03:K6;

MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;

Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,

Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,

Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;

"Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae.";

Lancet 361:743-749(2003).

Lancet 361:743-749(2003).

-!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Fe-S clusters in biosynthetic enzymes (By similarity).

repair of Fe-S clusters in biosynthetic enzymes (By similarity).
                                                                          Genome Res. 13:2577-2587(2003).

Genome Res. 13:2577-2587(2003).

-!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).

-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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/FTId=PRO 0000214512.
7EA0CB75840A255C CRC64;
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S.-F.;
vulnificus,
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Mismatches
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Pred. No. 3
                         Vibrio
                                                                                                                                                                                                                                                                                                                                            GenomeReviews; BA000037 GR; VV2885.
BioCyc; VVUL196600:VV2885-MONOMER; -.
HAMAP; MF 00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PF04362; Iron traffic; 1.
PIRSF; PIRSF029827; Fe traffic YggX; 1
ProDom; PD029191; DUF495; 1.
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 Shao C.-P., Lee C.-T., Hor L.-I
"Comparative genome analysis of
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GenomeReviews; BA000031_GR;
HAMAP; MF_00686; -; 1.
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Best Local Similarity 82.2.
T4; Conservative
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Bacteria; Proteobacteria;
Vibrionaceae; Vibrio.
NCBI_TaxID=670;
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                                                       pathogen.";
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                                                                                                                                                        1 MSRTIFCTFLOREAEGODFOLYPGELGKRIYNEISKBAWAQWQHKQTMLIN
                                                                                                                                                                   CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which
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Distributed under the Creative Commons Attribution-NoDerivs
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Vibrio alginolyticus 12G01.
Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
Vibrionaceae; Vibrio.
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                                                         Probable Fe(2+)-trafficking /FTId=PRO_0000214510.
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                                                                                  CRC64;
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                                                                                                        DB 1;
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Pred. No. 9.7e-33;
3; Mismatches
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                                                                                                       Score 399; DB 1, Pred. No. 6e-33; 7; Mismatches
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Remington K., Beeson K., Tran B., Rogers Y
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Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe traffic_YggX;
ProDom; PD029191; DUF495; 1.
Hypothetical protein.
SEQUENCE 90 AA; 10629 MW; A75D0C5
InterPro; IPR007457; YggX.
Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe_traffic_YggX;
ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                       EHRKLLEQEMVNFLFEGKEVHIEGYTP
                                                                                                                                                                                                                   EHRKLLETEMVNFLFEGKDVHIEGYTP
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                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                             16-MAY-2006, integrated into Un
16-MAY-2006, sequence version 1
11-JIII,-2006, entry version 3.
Hypothetical protein.
ORFNames=V12G01_14084;
                                                                                                                              7;
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illarity 82.8%;
Conservative
                                                                                  10629 MW;
                                                                                                        82.1%;
                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                     . Similarity 83.973; Conservative
                                                Iron
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                                           Complete proteome; CHAIN
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                                                                                  90 AA;
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NCBI_TaxID=314288
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STRAIN=12G01;
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16-MAY-2006,
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Submitted (
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STRAIN=91001 / Biovar Mediaevalis;

RubMed=1536893; DOI=10.1093/dnares/11.3.179;

Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D., A Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z., A Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J., A Yang H., Wang J., Huang P., Yang R.;

"Complete genome sequence of Yersinia pestis strain 91001, an isolate a virulent to humans.";

I DNA Res. 11:179-197(2004).

C -!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).

C -!- SUBUNIT: Monomer (By similarity).
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Distributed under the Creative Commons Attribution-NoDerivs License
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Yu J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLECTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=KIM5 / Biovar Mediaevalis;
MEDLINE=22137863; PubMed=12142430;
DOI=10.1128/JB.184.16.4601-4611.2002;
Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P. Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.
                                                                                                                                                                                                                                              MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G., Prentice M.B., Sebaihia M., James K.D., Churcher C.M., Mungall K.L., Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M., Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G., Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V., Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.; "Genome sequence of Yersinia pestis, the causative agent of plague." Nature 413:523-527(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Probable Fe(2+)-trafficking protein /FTId=PRO 0000214519.
                                                                                                                                                     Enterobacteriales
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Monomer (By similarity).
SIMILARITY: Belongs to the Fe(2+)-trafficking protein family
                                      into UniProtKB/Swiss-Prot
                                                                                                                                                      Gammaproteobacteria;
                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA]
STRAIN=CO-92 / Biovar Orientalia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enome sequence of Yersinia pestis KIM.";
Bacteriol. 184:4601-4611(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genomic_DNA
                                                         01-MAR-2002, sequence version 1.
11-JUL-2006, entry version 30.
Probable Fe(2+)-trafficking protein.
OrderedLocusNames=YPO0953, y3340, YP3488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HAMAP; MF_00686; -; 1.
InterPro; IPR007457; Yggx.
Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe_traffic_Yggx;
ProDom; PD029191; DUF495; 1.
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YPO0953.
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GenomeReviews; AE009952 GR; y3340.
GenomeReviews; AE017042 GR; YP3488.
GenomeReviews; AL590842 GR; YP3488.
BioCyc; YPES187410:Y3340-MONOMER; -
BioCyc; YPES632:YP00953-MONOMER; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Straley S.C., McDonough K.A.,
Perry R.D.;
                                                                                                                                                Bacteria; Proteobacteria; Gam
Enterobacteriaceae; Yersinia.
                                      integrated
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al protein.
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NCBI_TaxID=343509;
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US DOE Joint Genome Institute;
Barry K., Lucas S., Lapidus A., Copeland A., Detter J.C.,
Glavina del Rio T., Hammon N., Dalin E., Tice H., Pitluck S.,
Chain P., Hu P., Malfatti S.A., Radnedge L., Vergez L.M., Larimer
Land M., Hauser L., Worsham P., Chu M.C., Andersen G., Richardson
"Complete sequence of chromosome of Yersinia pestis Nepal516.";
Submitted (APR-2006) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                Gammaproteobacteria; Enterobacteriales;
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                                                                                                                                                                                                                                                                                                               STRAIN=Nepal516,
PubMed=16740952; DOI=10.1128/JB.00124-06;
Chain P.S., Hu P., Malfatti S.A., Radnedge L., Larimer F.,
Vergez L.M., Worsham P., Chu M.C., Andersen G.L.;
"Complete Genome Sequence of Yersinia pestis Strains Antiqua Nepal516: Evidence of Gene Reduction in an Emerging Pathogen J. Bacteriol. 188:4453-4463 (2006).
                              Length 90;
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         CRC64;
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                       DB 1; LE
1.2e-32;
8;
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Pred. No. 1.2e-32;
3; Mismatches B;
 c -> G (in Ref. 3)
C7374E6855653F65
                                                                                                                                                                                                    11-JUL-2006, integrated into UniProtKB/TrEMBL 11-JUL-2006, sequence version 1. 11-JUL-2006, entry version 1. Hypothetical protein.
                            Score 396; DB Pred. No. 1.2e 8; Mismatches
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nilarity 82.2%;
Conservative 8
         10707 MW;
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Enterobacteriaceae, Yersinia
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82.2%;
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Hypothetical protein.
ORFNames=YPN 3151;
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74; Conserv
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QICB93 YERPE
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Distributed under the Creative Commons Attribution-NoDerivs License
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-!- FUNCTION: Could be a mediator in iron transactions between iron
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Sodalis glossinidius (strain morsitans).
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales
Enterobacteriaceae; Sodalis.
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                                                                                                                                                                                                                                                                                                                                                             Chain P.S., Hu P., Malfatti S.A., Radnedge L., Larimer F., Vergez L.M., Worsham P., Chu M.C., Andersen G.L.; "Complete Genome Sequence of Yersinia pestis Strains Antiqua Nepal516: Evidence of Gene Reduction in an Emerging Pathogen. J. Bacteriol. 188:4453-4463(2006).
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PubMed=16365377; DOI=10.1101/gr.4106106;
Toh H., Weiss B.L., Perkin S.A.H., Yamashita A., Oshima K.,
Hattori M., Aksoy S.;
"Massive genome erosion and functional adaptations provide into the symbiotic lifestyle of Sodalis glossinidius in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIRAIN-AMERICANCE,
US DOB Joint Genome Institute;
Copeland A., Lucas S., Lapidus A., Barry K., Detter J.C.,
Glavina del Rio T., Hammon N., Dalin E., Tice H., Pitluck
Glavina del Rio T., Malfatti S.A., Radnedge L., Vergez L.M.,
Chain P., Hu P., Malfatti S.A., Chu M.C., Andersen G.L.,
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Submitted (APR-2006) to the EMBL/GenBank/DDBJ databases
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Pred. No. 1.2e-32;
1; Mismatches 8;
                                                                                                                                                                   Gammaproteobacteria;
integrated into UniProtKB/TrEMBL. sequence version 1.
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                                                                                                                                                                                                                                                                                                         STRAIN=Antiqua;
PubMed=16740952; DOI=10.1128/JB.00124-06;
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25-JUL-2006, entry version 6.
Probable Fe(2+)-trafficking protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US DOD Copeland A., Lucc. Glavina del Rio T., Hammer Chain P., Hu P., Malfatti S.A., R. Chain P., Hauser L., Worsham P., Clar,
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8
                                                                                                                   Yersinia pestis Antiqua.
Bacteria; Proteobacteria; Gar
Enterobacteriaceae; Yersinia
NCBI_TaxID=360102;
                                              11-JUL-2006, entry version 1 Hypothetical protein. ORFNames=YPA_0311;
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Best Local
                    SEQUENCE
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PubMed=15378067; DOI=10.1038/nbt1010;

Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,

Kim C.H., Jeong H., Hur C.G., Kim J.J.;

"The genome sequence of the capnophilic rumen bacterium Mannheimia
succiniciproducens.";

Nat. Biotechnol. 22:1275-1281(2004).

-!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or
repair of Fe-S clusters in biosynthetic enzymes (By similarity).

-!- SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.
and/or
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similarity)
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Gammaproteobacteria; Pasteurellales;
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                                                                                                                                                                                                                                                                                                                                      Probable Fe(2+)-trafficking pro/
/FTId=PRO_0000246119.
E9016C38ASD0S394 CRC64;
synthe
                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniproDistributed under the Creative Commons Attribution-NoDerivs
                                                                                                                                                                                                                                                                                                                                                                                                                      90;
              repair of Fe-S clusters in biosynthetic enzymes (By si SUBUNIT: Monomer (By similarity).
SIMILARITY: Belongs to the Fe(2+)-trafficking protein
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                                                                                                                                                                                                                                                                                                                                                                                                                      Score 390; DB 1;
Pred. No. 5.1e-32;
); Mismatches 7
 and iron-requiring processes,
                                                                                                                                                          EMBL; AP008232; BAE75311.1; -; Genomic_DNA.
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                                                                                                                                                                                                                                                      Pfam; PF04362; Iron traffic; 1.
PIRSF; PIRSF029827; Fe traffic_YggX;
ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 ADRKVLEQEMINFLFEGQDVHIQGYTP
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11-JUL-2006, entry version 12.
Probable Fe(2+)-trafficking protein.
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Pfam; PF04362; Iron traffic; 1.
PIRSF; PIRSF029827; Fe traffic ProDom; PD029191; DUF495; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                10;
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Bactería; Proteobacteria; Gam
Pasteurellaceae; Mannheimia.
                                                                                                                                                                                                                                                                                                                                                                                  10701 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                         80.2%;
80.5%;
                                                                                                                                                                                          GenomeReviews; AP008232_GR;
HAMAP; MF_00686; -; 1.
InterPro; IPR007457; YggX.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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HAMAP, MF 00686; -; 1
InterPro, IPR007457;
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CHAIN 1
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 acquisition
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25-OCT-2004,
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FETP_MANSM
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    d, strain KW20.";
    J. Bacteriol. 187:4627-4636(2005).
    J. Bacteriol. 187:4627-4636(2005).
    FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-requiring processes, such as synthesis and/or repair of Fe-S clusters in biosynthetic enzymes (By similarity).
    SIMILARITY: Belongs to the Fe(2+)-trafficking protein family.

                                                                                                                                          MSRTIFCTFLQREAEGODFQLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKKLNMMNA
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/FTId=PRO_0000246101.
EB34CEFF7737B93B_CRC64;
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Bakaletz
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Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
Pasteurellaceae; Haemophilus.
NCBI_TaxID=281310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nontypeable
I. influenzae
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                                                                                       Indels
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PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
Harrison A., Dyer D.W., Gillaspy A., Ray W.C., Mungur R.,
Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L.,
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                                                   ore 389; DB 1;
ed. No. 6.5e-32;
Mismatches 8
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Pred. No. 1e-31;
2; Mismatches
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HAMAP; MF_00686; -; 1.
InterPro; IPR007457; YggX.
Pfam; PF04362; Iron_traffic; 1.
PIRSF; PIRSF029827; Fe_traffic_YggX;
ProDom; PD029191; DUF495; 1.
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11-JUL-2006, entry version 7.
Probable Fe(2+)-trafficking protein.
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ilarity 78.4%;
Conservative 1
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Similarity 78.2%;
68; Conservative
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Search completed: June 27, 2007, 11:10:39 Job time : 349 secs

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- 2007
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protein search, using sw model OM protein

Search time 50 Seconds (without alignments) 159.306 Million cell 1 11:10:57 2007, 27, June Run on:

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486 1 MSRTIFCTFLQREAEGQDFQ.... score: Perfect so Sequence:

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650591 seqs, 87530628 residues Searched:

Total number of hits satisfying chosen parameters

650591

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

		Description	1962 Sequence 11962,	443 Sequence 5443,	3355 Sequence 233	56 Sequence 5456,	59 Sequence 2859,	3, App	4473 Sequence 24473,	Sequence 24, Ap	6 Sequence 66, Ap	Sequence 2, App	2, App	2, App	Sequence 2, App	Sequence 2, App	Sequence 2, App	2, App	2, App	5 Sequence 95, Ap	Sequence 95, Ap	Sequence 95, Ap	Sequence 95, Ap	7 Sequence 97, Ap	7 Sequence 97, Ap	7 Sequence 97, Ap	Sequence 97, Ap	
SUMMARIES		QI	0	-09-543-681A-	52-9	-09-328-352-5	40-23	-167-299-	-09-252-991A-	-10-164-595-2	-325-93	-08-533-669A-	-09-183-861-	-09-022-76	-09-551-974A-	-09-565-5	-09-639-206A-	-09-874-923-	-08-79	-09-551-974A-	-09-565-501	-639-20	-874-923-9	51-97	-565-501A-	-09-639-20	-874-923-9	0 4400 133 00 011
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-09-565-501A-96 -09-639-206A-96 -09-874-923-96 -09-914-098-46 -09-252-991A-20905 -09-270-767-58283 -09-270-767-58283 -09-370-767-42959 -09-370-368-8	-09-540-236-2250 -09-107-532A-6689 -09-134-000C-4346 -09-248-796A-18911 -09-861-451A-12 -09-543-681A-6879 -09-248-796A-19555 -09-710-279-2850 -09-134-001C-3945 -09-562-737-124 -09-562-737-125	US-09-298-924-4 US-08-840-236-1 US-08-505-448A-1 US-09-198-452A-1004 US-09-438-185A-934 US-09-513-999C-4802 US-09-513-999C-4800 US-09-949-016-6012 US-09-914-098-48	-10-243-735-2 -10-730-010-2 -09-171-991-7 -09-270-767-41085 -09-270-767-61671 -09-248-796A-19265 -09-198-452A-221 -09-438-185A-205 -09-328-352-6400 -09-270-767-46116
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## ALIGNMENTS

US-09-489-039A-11962
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Sequence 11962, Application US/09489039A
GENERAL INFORMATION:
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: WUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: WUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR PILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107 Klebsiella pneumoniae ; TYPE: PRT ; ORGANISM: Klebsi US-09-489-039A-11962

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Sequence 2859, Application US/09540236
Sequence 2859, Application US/09540236
Batent No. 6673910
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
ATITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARITILE REFERENCE: 2709.2005-001
CURRENT APPLICATION NUMBER: US/09/540,236
CURRENT FILING DATE: 2000-04-04
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2859
LENGTH: 110
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                                                                                                                                                                 Sequence 5456, Application US/09328352
Sequence 5456, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5456
LENGTH: 92
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1.2e-08;
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Pred. No. 2.
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Pred. No.
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                                                                 EHRKLLEQEMVNFLFEGKEVHIEGYTP
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US-09-328-352-5456
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ilarity 34.9%;
Conservative 1:
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Best Local Similarity 42.7%;
Matches 38; Conservative
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29; Conserv
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Best Local S
Matches 29
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ORGANISM:
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S-09-543.

S-09-50.

GENERAL INFORMATION:

APPLICANT: GARY BRETON

TITLE OF INVENTION:

DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709.1002-001

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR PILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 5443

LENGTH: 93

LENGTH: 93
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S-09-252-991A-23355
Sequence 23355, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
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             Length 107
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            Score 450; DB 2;
Pred. No. 1.1e-48;
; Mismatches 3
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Pred. No. 4.2e-41
7; Mismatches 1
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                                                                                                                                                      61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK 91
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NUMBER OF SEQ ID NOS: 33142
EQ ID NO 23355
LENGTH: 122
              92.6%;
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llarity 80.0%;
Conservative
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                                                Conservative
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Best Local Similarity
Matches 45; Conser
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Matches 72; Conser
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               Query Match
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SEQ ID NO 2
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34; Conserv
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                                                                                                                     O ID NO 24
LENGTH: 1214
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Best Local S
Matches 23
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US-10-164-595
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Best Local (
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                                                                                                        SOFTWARE:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                               3 RTIFCTFLOREAEGODFOLYPGELGKRIYNEISKEAWAQ-WQH-KQTWLINEKKLNMMNA
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                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                           Synthetase DNA
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                                                                                                                                                                                                                                                                                                                    15.6%; Score 76; DB 2 llarity 30.7%; Pred. No. 0.77; Conservative 16; Mismatches
                                        APPLICANT: Kron, Micheal
APPLICANT: Hartlein, Micheal
APPLICANT: Hartlein, Micheal
APPLICANT: Michito, Hirikata
TITLE OF INVENTION: Human Asparaginyl-tRNA Sy
FILE REFERENCE: Aparaginyl-tRNA Synthetase
CURRENT APPLICATION NUMBER: US/09/167,299
CURRENT FILING DATE: 1998-10-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          103
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PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 24473
LENGTH: 474
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -- AKMLEKDATEVGVKAALEEAKKVQIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24473, Application US/09252991A Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
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; Sequence 24, Application US/10164595
; Patent No. 6657054
3, Application US/09167299 . 6245539
                                                                                                                                                                                                                            ORGANISM: Brugia malayi
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: P10723
DATABASE ENTRY DATE: 1997-11-01
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iilarity 25.6%;
Conservative 1
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Best Local Similarity
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hes 20; Conser
Sequence 3, Applicat
Patent No. 6245539
GENERAL INFORMATION:
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Best Local S
Matches 20
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              Genes and Polypeptides
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                                                                                                                                                                                     Length 1214;
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the modification
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LEISHMANIA ANTIGENS FOR
THERAPY AND DIAGNOSIS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 67.5; D
Pred. No. 2.1;
4; Mismatches
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APPLICANT: Origene Technologies, inc
TITLE OF INVENTION: Regulated Anglogenesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFLOREAEGOD-FOLYPGELGKRIYNEISKE-
                                                                                                                                                                                        70.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/325,93.
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 206
             TITLE OF INVENTATION 103 R1
CURRENT APPLICATION NUMBER: US/10/164,
CURRENT FILING DATE: 2002-06-10
                                                                                                                                                                                      Score 'Pred. 1
                                                                                                                                                                                                                                                                                                                                                                                                66, Application US/09325932A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                equence 2, Application US/08533669A atent No. 5834592 GENERAL INFORMATION:
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                                                                                                                                                                                      14.5%;
28.4%;
                                                                     NUMBER OF SEQ ID NOS: 80
SOFTWARE: PatentIn version 3
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APPLICANT:
APPLICANT:
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CITY: S
STATE:
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Best Local
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                                                                              COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                  701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 67.5; DB Pred. No. 8.9; 2; Mismatches
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                                                                                                                                                                                                                                                                                                             31,392
3R: 210121.420
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               ADDRESSEE: SEED and BERRY LLP STREET: 6300 Columbia Center,
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                                                                                                                                                                                                                                                                                           NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 MTRNALCLORORKYEAA-IDLY-
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; Sequence 2, Application US/09183861
; Patent No. 6365165
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
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Best Local Similarity 28.3%;
Matches 26; Conservative
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APPLICATION NUMBER: US/(FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                        546 amino acids
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CORRESPONDENCE ADDRESS:
                                                                   Washington
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STATE: Washing
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US-08-533-669A-2
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Campos-Neto, Antonic
Webb, John R.
Dillon, Davin C.
Skeiky, Yasir A.W.
Skeiky, LEISHMANIA ANTIGENS FOR USEIN THE THERAPY AND
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                                                                                                                                                                                                                                                                                                                                               Indels
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          EHRKLLEQEMVNFLFEGKEVHIEG--YTPEDK
                                                                      31,392
3R: 210121.420C3
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APPLICATION NUMBER: US/09/022,765
FILING DATE: 12-FEB-1998
                                                NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 2101
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 546 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                       301 MTRNALCLORORKYBAA-IDLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2, Application US/0902276:
Patent No. 6375955
GENERAL INFORMATION:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
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Similarity 28.3%;
26; Conservative
                                  ATTORNEY/AGENT INFORMATION:
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nino acid
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amino acid
                                                                                                                                                                                                                                                       protein
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TITLE OF INVENTION: LE:
NUMBER OF SEQUENCES: 8'
CORRESPONDENCE ADDRESS:
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NUMBER
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OPERATING SYSTEM:
                                                                                                                                                                                                                                      linear
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ZIP: 98104-7092
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MOLECULE TYPE:

US-09-183-861-2
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2001-06-04
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28.3%;
                        th 13.9%;
Similarity 28.3%;
26; Conservative 1
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APPLICATION NUMBER:
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Campos-Neto, A.
Webb, John R.
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Skeiky, Yasir
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FastSEQ for
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                                                                                                                                                                                                                                                   INFORMATION:
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CURRENT APPLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-639-206A-2
  US-09-565-501A-2
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
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CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 8.9;
12; Mismatches
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Webb, John R.
Dillion, Davin C.
Skeiky, Yasir A.W.
Bhatia, Ajay
Coler, Rhea
Peter Probst
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illarity 28.3%;
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OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
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TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF ILE REFERENCE: 210121.420C7
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Campos-Neto, Anton:
Webb, John R.
Dillion, Davin C.
Skeiky, Yasir A.W.
Bhatia, Ajay
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OF SEQ ID NOS: 122
RE: FastSEQ for Windows Version 4.0
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
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; Sequence 2, Application US/08798841
: Patent No. 6709661
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
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                                                             ; ORGANISM: Leishmania major
US-09-874-923-2
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TITLE OF INVENTION: LEIS
TITLE OF INVENTION: THER
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
                                                                                                                 Similarity 28. 26; Conservative
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APPLICATION NUMBER: US
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GENERAL INFORMATION:
APPLICANT: Corixa
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CITY: Seattle
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LENGTH: 546
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                                                 APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEI
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Pred. No. 19;
2; Mismatches
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Pred. No. 19;
2; Mismatches
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CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                    US/09/551,974A
                                                                                                                                                                                                                                                                                                                                         Fusion (poly-protein)
Leishmania antigens
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OTHER INFORMATION: Leishmania antigens
09-565-501A-95
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 101
SOFTWARE: FastSEQ for Windows Version
95, Application US/09551974A
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CURRENT APPLICATION NUMBER: US/0
CURRENT FILING DATE: 2000-04-14
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Conservative 12;
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Webb, John R.
Dillion, Davin C.
Skeiky, Yasir A.W.
Bhatia, Ajay
Coler, Rhea
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ORGANISM: Artificial Sequence
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larity 28.3%;
Conservative
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Best Local Similarity
Matches 26; Conser
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US-09-551-974A-95
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TITLE OF INVENTION:
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                                   GENERAL INFORMATION:
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Score 67.5;
Pred. No. 1
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Leishmania antigens
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Webb, John R.
Dillion, Davin C.
Skeiky, Yasir A.W.
Bhatia, Ajay
                              ORGANISM: Artificial Sequence
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Best Local Similarity
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INFORMATION:
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US-09-551-974A-97
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GENERAL INFORMATION:
APPLICANT: Reed, S
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APPLICANT: Reed, S
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SOFTWARE: FABI
SEQ ID NO 97
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                   ---KRALVEWRNPDTL-
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
APPLICANT: Probst, Peter
APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
                                                                                                                                                                                                                                                                                                               CANT: Coler, Rhea CANT: Peter CANT: Probst, Peter OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
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Pred. No. 19;
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TITLE OF INVENTION: LEISHMANIA ANTIGENS FOI
TITLE OF INVENTION: THERAPY AND DIAGNOSIS
FILE REFERENCE: 210121.420C7
CURRENT APPLICATION NUMBER: US/09/639,206A
CURRENT FILING DATE: 2000-08-14
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FastSEQ for Windows Version 4.0
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SOFTWARE: FastSEQ for Windows Version 4.0
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Patent No. 6638517
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                              509 MTRNALCLORORKYEAA-IDLY-
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APPLICANT: Campos-Neto, Antoni
APPLICANT: Webb, John R.
APPLICANT: Dillion, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Bhatia, Ajay
APPLICANT: Coler, Rhea
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illarity 28.3%;
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CURRENT APPLICATION NUMBER: 1
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Campos-Neto, Ar
Webb, John R.
Dillon, Davin C.
Skeiky, Yasir P.
Bhatia, Ajay
Coler, Rhea
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                                                                                                                                                                      Sequence 95, Applica Patent No. 6613337 GENERAL INFORMATION:
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APPLICANT: Reed, St.
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ENGTH: 982
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Leishmania antigens
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APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Webb, John R.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C5
CURRENT APPLICATION NUMBER: US/09/551,974A
                                          - KRALVEWRNPDTL
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Pred. No. 32;
2; Mismatches
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APPLICANT: Probst, Peter
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
FILE REFERENCE: 210121.420C7
CURRENT APPLICATION NUMBER: US/09/639,206A
CURRENT FILING DATE: 2000-08-14
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Fast SEQ for Windows Version 4.0
LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND DIAGNOSIS OF LEISHMANIASIS
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OTHER INFORMATION: Leishmania antigens
-09-565-501A-97
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Pred. No. 32;
12; Mismatches
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                              FILE REFERENCE: 210121.420C6
CURRENT APPLICATION NUMBER: US/09/565,501A
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 112
SOFTWARE: FastSEQ for Windows Version 4.0
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OTHER INFORMATION: Leishmania antigens
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Patent No. 6613337
                                                                                                                                                                                                                                                                                                                                                                              509 MTRNALČLQRORKYBAA-IDLY--
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                                                                                                                                                                                                                                                                           th 13.9%; Sc. Similarity 28.3%; Pr 26; Conservative 12;
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APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonic
APPLICANT: Webb, John R.
APPLICANT: Dillion, Davin C.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Shatia, Ajay
APPLICANT: Coler, Rhea
                                                                                                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
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TITLE OF INVENTION: TITLE OF INVENTION:
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LENGTH: 1427
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US-09-874-923-97
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Pred. No. 32;
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Leishmania antigens
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FastSEQ for Windows Version
Application US/09874923
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                                                                                                                                                                     APPLICANT: Brannon, Mark
TITLE OF INVENTION: LEISHMANIA
TITLE OF INVENTION: THERAPY AN
FILE REFERENCE: 210121.420C8
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28.3%;
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iky, Yasir
tia, Ajay
                                                Steven G
                                                                                                                                                           Peter
                                                              Campos-Neto,
Webb, John R
                                                                                                            Skerra
Bhatia, Ayra
Jar, Rhea
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LENGTH: 1427
TYPE: PRT
ORGANISM: Artificial 8
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26; Conserv
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                               GENERAL INFORMATION: APPLICANT: Reed, St
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.....NFLFEGKEVHIEGYTPEDKK 1 MSRTIFCTFLQREAEGQDFQ... US-09-955-502A-11 486 score: Perfect

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Sequence:

residues 2097797 seqs, 463214858 Searched:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

		æ			SUMMAKIES	
Result No.	Score	Query Match	Length	DB	ΩΙ	Description
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ence 28, App	equence 29. App	equence 30, App	equence 31, App	equence 32, A	ر 4 کار 1	equence 66021,	equence 18744,	equence 2028,	equence 105, A	equence 862, A	equence 37, Ap	equence 15, Ap	equence 4885,	equence 144,	equence 24, Ap	ence 400, A	equence too, a	equence 34, Ap	equence 180, A	equence 169643	equence 24705	equence 189166,	equence 36, App	equence 2088, A	equence 52, App	equence 768, Ap	equence 66, App	equence 118, Ap	equence 9369, A		equence 71. App	equence 128, Ap	e 127, Ap	equence 95, App	equence 95, App	equence 97, App	equence 97, App	equence 96, App	equence 96, App	equence 16266,	equence 6155, A	equence 6154, A	270,
09-955-502	-T0-49/-93/-38	8-09-955-502-3	55-50	5-09-955-502-32	US-IU-450-763-4IIUY IIS-10-282-1224-68134	S-10-282-122A-660	S-10-369-493-1874	-11-087-099-20	5-10-805-684-10	8-10-506-454-86	-10-416-330-3	8-10-491-467-15	5-10-732-923-48	S-10-085-198-1	S-IO-/I/-665-24	4500-00-	0-10-22-008A-10	-10-23-00/-04 -10-274-700%:20	10-225-0668-1	-10-437-963-169 -10-437-963-169	-11-097-143-24705	S-10-437-963-189	-10-415-478A-36	-10-47	-10-393-840-52	-09-864-408A-	-10-219-220-66	S-10-393-840-118	-10-732-923-93	US-U9-8/4-923-2 TE-00-001-406-2	S-10-098-732A-7	-09-991-496	-09-991-496-12	S-09-874-923-	-09-991-496-9	S-09-874-923-9	-09-991-496-9	-09-874-923-9	-09-991-496-96	S-11-188-298-1626	-11-096-568A-	S-11-096-568A-615	-10-425-114-4457
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## ALIGNMENTS

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Sequence 11, Application US/09955502

Sequence 11, Application US/09955502

Sequence 11, Application US/09955502

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Grainick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 11

LENGTH: 91

TYPE: PRT

CORGANISM: Escherichia coli K-12 MG1655
                              US-09-955-502-11
RESULT 1
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Similarity 100
91, Conservative
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86; Conserv
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US-09-955-502-16
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SOFTWARE: Par
SEQ ID NO 16
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LENGTH: 91
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Batent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1
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                                 Score 486; DB 3;
Pred. No. 7.9e-47
Mismatches 0
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US-09-955-502-13

Sequence 13, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superint of Invention: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 13

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US-09-955-502-12
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 7.9e-47
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ed. No. 6.5e-45;
Mismatches 0
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6.5e-45;
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APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superitre OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILLING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing SuperITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
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Pred. No. 7. Mismatches
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Pred. No. 6
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Patent No. US20020072118A1
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Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
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US-09-955-502-14
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SOFTWARE: PatentIn Ver. (
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| 86; Conser
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Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2000-09-22
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Pred. No. 6.5e-45;
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Pred. No. 2.5e-43;
5; Mismatches 2;
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Sequence 17, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superitre OF INVENTION: Oxygen-Labile Proteins

TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1
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                                                                                    61 EHRKLIBQEMVSFLFEGKDVHIEGYTPEDKK
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US-09-955-502-17
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ilarity 92.3%;
Conservative
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illarity 94.5%;
Conservative
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 18
LENGTH: 91
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LENGTH: 91
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Best Local S
Matches 84
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                                                                                                                                                                Preventing Superoxide Damage
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            EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
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APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Prevent; TITLE OF INVENTION: Oxygen-Labile President Reference: 960296.97559
                                                                                                                                                              2001-09-18
PRR: 60/234,588
                                                                                             15, Application US/09955502 or. US20020072118A1
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                                                                                                                      GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for P
TITLE OF INVENTION: Oxygen-Labi
FILE REFERENCE: 960296.97559
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Similarity 94.3%;
83; Conservative
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SOFTWARE: PatentIn Ver.
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; ORGANISM: Vil
US-09-955-502-10
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LENGTH: 90
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Best Local S
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Sequence 19, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Grainick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502
                                                                                                                   APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
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Pred. No. 1.1e-36;
; Mismatches
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61 EHRKLLEQEMVNFLFEGKEVHIEGYTPPAK
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PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
                                                                      Sequence 20, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
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US-09-955-502-19
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82.2%;
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                                                                                                                                                                                                                                          FILING DATE: 2000-09-22
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                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Yersinia pestis
US-09-955-502-20
                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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Best Local Simi
                                                           US-09-955-502-20
                                                                                                                                                                                                                                                                                                    LENGTH: 90
TYPE: PRT
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LENGTH: 78
                                                                                                                                                                                                                                                                                     SEQ ID NO 20
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Best Local S
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Sequence 5, Application US/09955502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Dar

TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                             , DB 3;
8.7e-36;
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                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Actinobacillus actinomycetemcomitans
                                                                                                                                                                                                                                                                                                                                                          Score 388; DB Pred. No. 8.7e 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 EHRKLLEQEMVNFLFEGKEVHIEGYTPEDKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 EHRKLLEQEMVNFLFEGKDVHIEGYTPPEAK
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APPLICANT: Downs, Diana M.
TITLE OF INVENTION: Method for Preven; TITLE OF INVENTION: Oxygen-Labile Print REFERENCE: 960296.97559; CURRENT APPLICATION NUMBER: US/09/955; CURRENT FILING DATE: 2001-09-18; PRIOR FILING DATE: 2000-09-22
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; ORGANISM: Haemophilus influenzae
US-09-955-502-7
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ilarity 76.9%;
Conservative 1:
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ilarity 78.2%;
Conservative 12
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SOFTWARE: Patentin Ver.
SEQ ID NO 7
LENGTH: 87
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US-09-955-502-6
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RESULT 17
US-09-955-502-21
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ENGTH: 76
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Best Local S
Matches 47
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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                                                               Superoxide Damage
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Pred. No. 8.5e-35;
4; Mismatches 7;
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Pred. No. 4.1e-34;
; Mismatches 9;
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing SuperITTLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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5-09-955-502-9
Sequence 9, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 8, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                             78.0%;
ilarity 75.9%;
Conservative 14
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Best Local Similarity
Matches 66; Conser
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APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 1.7e-29
2; Mismatches 16
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
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Pred. No.
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APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing of The Second Second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Shewanella putrefasciens
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Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
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68.2%;
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61.8%;
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SOFTWARE: Patentin Ver.
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APPLICATION NUMBER:
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SOFTWARE: Pat
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ENGTH: 87
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; Fatent No. US20020072116A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cel
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-22
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Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
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Pred. No. 8.1e-21;
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                US/09/955,502
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JER: 60/234,588
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US-09-955-502-2
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                                                     NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
 FILE REFERENCE: 960296.97559
           CURRENT APPLICATION NUMBER:
CURRENT FILING DATE: 2001-C
PRIOR APPLICATION NUMBER: 60
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SOFTWARE: PatentIn Ver. 2.1
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ENGTH: 87
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APPLICANT: Grainick, Jeff A.
AFFLICANT: Grainick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILLING DATE: 2000-09-22
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TITLE OF INVENTION: Method for Preventing Superoxide Damage
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
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Pred. No. 3
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60/234,588
60/234,588
                                                                                                                           ORGANISM: Bordetella bronchiseptica
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Patent No. US20020072118A1
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No. US20020072118A1
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US-09-955-502-25
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larity 51.7%;
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GENERAL INFORMATION:
APPLICANT: Downs, Diana M
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PRIOR FILING DATE: 2000-0
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                                 SEQ ID NOS: PatentIn Ver
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; TYPE: PRT
; ORGANISM: Xylella
US-09-955-502-22
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LENGTH: 87
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Sequence 23, Application US/09955502

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cel

TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

CURRENT FILING DATE: 2001-09-18

PRIOR FILING DATE: 2000-09-22

NUMBER OF SEQ ID NOS: 33

SOFTWARE: Patentin Ver. 2.1
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Sequence 22, Application US/09955502

Sequence 22, Application US/09955502

Batent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502
                                                                                                          Length 88;
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2000-09-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Pseudomonas syringae
US-09-955-502-23
                                                             Coxiella burnetii
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PRIOR FILING DATE: 2000-05
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SOFTWARE: PatentIn Ver.
SOFTWARE: Patentin Ver. IEQ ID NO 33 LENGTH: 88
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Best Local Similarity
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SEQ ID NO 22
LENGTH: 89
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LENGTH: 90
                                               TYPE: PRT
                                                           ; ORGANISM:
US-09-955-502
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APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
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                                             Length 89
                                                                             Indels
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Pred. No. 1.9e-17;
); Mismatches 29
                                             , DB 3;
1.5e-17
                                             Score 226; DB Pred. No. 1.5e 0; Mismatches
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                                                                                                                                                                                                                                                                              Sequence 24, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
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Best Local Similarity
Matches 45; Conser
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Title:

US-09-955-502A-11 486 Perfect score:

1 MSRTIFCTFLOREAEGODFQ......NFLFEGKEVHIEGYTPEDKK Sequence:

table: Scoring

0.5 BLOSUM62 Gapop 10.0 , Gapext residues 1408788 segs, 343594471 Searched:

1408788 of hits satisfying chosen parameters Total number

length: 0 length: 2000000000 seq seq Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 75 summaries

Database

Published Applications AA New: \*

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EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB.pep: ' 10m4n9r8

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## SUMMARIES

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31	! !	47.5	I N		US-10-419-128-233	equence	3355,
			Н	Ø	-10-603-108-285	equence	59,
•			Н	7	16-230-4431	equence	4315,
			0	7	-11-516-230-4428	equence	283,
			0	7	6-230-4429	equence	299,
			0	7	-11-516-230-4426	equence	63,
		•	546	7	-11-516-230-442	_	N
			0	7	-11-516-230-4427	equence	271,
		Ŋ.	O	9	-10-526-324-	equence	6, A
		4.	7	9	19-128-244	equence	473,
		4	O	7	-11-516-230-4426	equence	261,
٠		4.	Н	9	3-032-1188	Sequence 1	118890,
•		4	9	9	-10-276-817B-1293		σ
•		4	8	9	-10-917-503-110	Sequence 1	063,
0.5			Н	7	-11-443-428A-890	equence	03
•		4.	Н	7	-11-443-428A-89038	equence	038
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•		4.	4	7	-11-443-428A-8	ednence	90383
•		4.	O	9	-405-027-332	equence	29, A
•		4	9	,	1-667	equence	~
•		4.	σ	7	1-667	equence	75, A
•		4	07	7	037	equence	90379,
•		4	7	7	8A-89	equence	890395,
٠		4.	10	7	039	equence	039
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S-11-443-428A-89 S-11-443-428A-89 S-11-443-428A-89 S-11-443-428A-89 S-11-443-428A-89	-11-443-428A-89039 -11-443-428A-89038 -11-443-428A-89039 -11-443-428A-89039 -11-582-861-6674 -11-582-861-6672	S-11-582-861-6673 S-11-443-428A-8903 S-11-443-428A-8610 S-11-443-428A-8610 S-11-443-428A-8610 S-11-443-428A-8610 S-11-375-241-64	S-11-371-354-7416 S-11-371-354-7416 S-11-443-428A-861 S-11-443-428A-861 S-11-443-428A-861 S-11-516-230-4436 S-11-443-428A-861	-11-443-428A-86101 -10-953-349-11813 -10-953-349-11812 -10-953-349-11811 -11-486-448-69349 -11-516-230-44341 -11-516-230-44257 -11-516-230-44257 -11-516-230-44257	US-10-474-894-15 US-10-760-320A-2528 US-11-582-861-7080 US-10-467-478-814 US-10-467-478-551 US-11-330-403-983 US-11-330-403-984 US-11-443-428A-965050 US-10-219-051B-1778 US-10-743-643-2143 US-11-388-595-4
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## ALIGNMENTS

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Sequence 23355, Application US/10419128
; Sequence 23355, Application US/10419128
; Publication No. US20070020624A1
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1099-04-21
; PRIOR APPLICATION NUMBER: US/09/252,991
; PRIOR FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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Schauwecker, Florian
Schauwecker, Florian
Schauwecker, Florian
Schauwecker, Florian
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NUMBER OF SEQ ID NOS: 73449
SOFTWARE: Biomax PatentTool according to PatentIN 3.1
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Pred. No. 2.2;
1; Mismatches
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EP 06110325.5
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38.88;
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2006-02-24
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FILING DATE: 2006-02-24
APPLICATION NUMBER: EP
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Herold, Manfred
Wendel, Birgit
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Puzio, Piotr
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FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 44315
LENGTH: 514
                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT ORGANISM:
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
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TERRLINMINA
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APPLICANT: Herold, Manfred
APPLICANT: Wendel, Birgit
APPLICANT: Kamlage, Beate
APPLICANT: Kamlage, Beate
APPLICANT: Schauwecker, Florian
APPLICANT: Looser, Ralf
TITLE OF INVENTION: Process for the production of fir
FILE REFERENCE: 13195-00014-US
CURRENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
PRIOR FILING DATE: 2006-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41;
                                                                                          47.5%; Score 231; DB 6; ]
llarity 51.7%; Pred. No. 3.4e-16;
Conservative 10; Mismatches 32;
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Pred. No. 7e-06;
13; Mismatches 4
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CURRENT FILING DATE: 2003-06-24
PRIOR APPLICATION NUMBER: US 09/540,263
PRIOR FILING DATE: 2000-04-04
PRIOR APPLICATION NUMBER: US 60/125,416
PRIOR FILING DATE: 1999-04-09
NUMBER OF SEQ ID NOS: 3840
SEQ ID NO 2859
LENGTH: 110
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Sequence 44315, Application US/11516230
Publication No. US20070118916A1
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Sequence 2859, Application US/10603108
Publication No. US20070010665A1
GENERAL INFORMATION:
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Puzio, Piotr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: M.catarrhalis
US-10-603-108-2859
                                             ; ORGANISM: Pseudomonas
US-10-419-128-23355
                                                                                                          Similarity 45; Conser
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Best Local Similarity
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SEQ ID NO 23355
LENGTH: 122
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APPLICANT: Looser, Ralf
TITLE OF INVENTION: Process for the production of fine chemical
FILE REFERENCE: 13195-00014-US
CURRENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
PRIOR APPLICATION NUMBER: EP 06110426.1
PRIOR FILING DATE: 2006-02-24
PRIOR APPLICATION NUMBER: EP 06110579.7
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Pred. No. 6.3;
6; Mismatches
   data removed
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Remaining Prior Application data removed
NUMBER OF SEQ ID NOS: 73449
SOFTWARE: Biomax PatentTool according to
SEQ ID NO 44299
LENGTH: 508
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NUMBER: EP 06110383.4
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NUMBER: EP 06110378.4
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APPLICATION NUMBER: EP 06110423.8
FILING DATE: 2006-02-24
APPLICATION NUMBER: EP 06110418.8
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APPLICATION NUMBER: EP 06110425.3
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EP 06110325.5
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                                                                           , ORGANISM: Pseudomonas putida KT2440
US-11-516-230-44283
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28.2%;
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Herold, Manfred
Wendel, Birgit
 g Prior Application
F SEQ ID NOS: 73449
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Best Local Similarity 28.2
Matches 22; Conservative
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Piotr
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LENGTH: 507
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APPLICANT: Schauwecker, Florian
APPLICANT: Looser, Ralf
TITLE OF INVENTION: Process for the production of fine chemicals
FILE REFERENCE: 13195-00014-US
CURRENT APPLICATION NUMBER: US/11/516,230
CURRENT FILING DATE: 2006-09-06
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UMBER: BP 06110367.7
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UMBER: BP 06110327.1
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; Sequence 44265, Application US/11516230
; Publication No. US20070118916A1
; GENERAL INFORMATION:
Sequence 44263, Application US/11516230 Publication No. US20070118916A1
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R FILING DATE: 2006-02-24
R APPLICATION NUMBER: EP 06
R FILING DATE: 2006-02-24
R APPLICATION NUMBER: EP 06
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APPLICATION NUMBER: EP 0
FILING DATE: 2006-02-24
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Similarity 30.2%;
19; Conservative 1
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                                                                       Puzio, Piotr
Blau, Astrid
Herold, Manfred
Wendel, Birgit
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US-11-516-230-44271
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SNGTH: 507
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ORGANISM:
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TITLE OF INVENTION: Process for the production of fine chemicals
FILE REFERENCE: 13195-00014-US
CURRENT APPLICATION NUMBER: US/11/516,230
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ICANT: Schauwecker, Florian
ICANT: Looser, Ralf
E OF INVENTION: Process for the production of fine chemical
REFERENCE: 13195-00014-US
ENT APPLICATION NUMBER: US/11/516,230
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Pred. No.
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APPLICATION NUMBER: EP 06110418.8
FILING DATE: 2006-02-24
APPLICATION NUMBER: EP 06110383.4
                                                                                                                                                                                       FILING DATE: 2006-02-28
APPLICATION NUMBER: EP 06110425.3
FILING DATE: 2006-02-24
APPLICATION NUMBER: EP 06110423.8
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US-11-516-230-44265
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Publication No. US20070118916A1
GENERAL INFORMATION:
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APPLICATION NUMBER: EP 06110327
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SEQ ID NOS: 73449
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ker, Florian
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NUMBER: EP 0
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Puzio, Piotr
Blau, Astrid
Herold, Manfred
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                                                     Kamlage, Beat
Schauwecker,
Looser, Ralf
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APPLICANT: Puzio, Piotr
APPLICANT: Blau, Astrid
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TITLE OF INVENTION: METHOD OF TARGETED GENE DISRUPTION, GENOME OF
TITLE OF INVENTION: HYPERTHERMOSTABLE BACTERIUM AND GENOME CHIP USING
TITLE OF INVENTION: THE SAME
FILE REFERENCE: 490051.401USPC
CURRENT APPLICATION NUMBER: US/10/526,324
CURRENT FILING DATE: 2005-02-28
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DR FILING DATE: 2006-02-24
DR APPLICATION NUMBER: EP 06110327.1
DR FILING DATE: 2006-02-23
DR APPLICATION NUMBER: EP 06110325.5
DR FILING DATE: 2006-02-23
APPLICATION NUMBER: EP 06110325.5
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LENGTH: 309
TYPE: PRT
ORGANISM: Thermococcus kodakaraensis KOD1
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Sequence 706, Application US/10
Publication No. US20060248617A1
GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/11/516,230
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SEQ ID NO 24473
LENGTH: 474
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; Sequence 24473, Application US/10419128
; Publication No. US20070020624A1
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEC
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS ANI
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/10/419,128
; CURRENT FILING DATE: 2003-04-21
; PRIOR APPLICATION NUMBER: US/09/252,991
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LOCATION: (1128517)..(1128518)
OTHER INFORMATION: n is a or c
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NAME/KEY: misc feature
LOCATION: (1128499)..(1128499)
OTHER INFORMATION: n is a or c
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NAME/KEY: misc feature
LOCATION: (1128505)..(1128506)
OTHER INFORMATION: n is a or c
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LOCATION: (1128539)..(1128540)
OTHER INFORMATION: n is a or c
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LOCATION: (1561400)..(1561400)
OTHER INFORMATION: n is a or c
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LOCATION: (1561477)..(1561477)
OTHER INFORMATION: n is a or c
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LOCATION: (1561545)..(1561545)
OTHER INFORMATION: n is a or c
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LOCATION: (1767941)..(1767941)
OTHER INFORMATION: n is a or c
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LOCATION: (839139)..(839139)
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ISOGAI, TAKAO
NISHIKAWA, TETSUO
HAYASHI, KOJI
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SEQ ID NOS: 19025
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                                                                     ; LOCATION: (400)..(436)
; OTHER INFORMATION: MYND;
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US-10-276-817B-12931
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FILING DATE: 2000-0
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LOCATION: (304)..(352)
OTHER INFORMATION: Int
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24; Conserv
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ISOGAI,
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                                                         NAME/KEY: DOMAIN
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                                APPLICANT: Zhou, Yihua
TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules
TITLE OF INVENTION: Plants
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Publication No. US20070060743A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
FILE REFERENCE: 21272-104
CURRENT APPLICATION NUMBER: US/10/276,817B
CURRENT FILING DATE: 2002-11-18
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US-10-703-032-118890
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Pred. No. 11;
.8; Mismatches
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CURRENT APPLICATION NUMBER: US/10/703,032
CURRENT FILING DATE: 2003-11-06
PRIOR APPLICATION NUMBER: 10/020,338
PRIOR FILING DATE: 2001-12-12
NUMBER OF SEQ ID NOS: 211164
SEQ ID NO 118890
LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/14827
PRIOR FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/577,408
                                                                                                                                                            US-10-703-032-118890
; Sequence 118890, Application US/10703032
; Publication No. US20070044171A1
; GENERAL INFORMATION:
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Similarity 25.6%;
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SOFTWARE: Custom
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Conner, Timothy W
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Masucci, James D.
Zhou, Yihua
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                 EAEGODFOLYP
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LENGTH: 566
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  INFORMATION: Intermediate filaments proteins domain identified INFORMATION: accession number BL00226B, p-value=6.337e-09, raw
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Mismatches
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Pred. No. 40;
0; Mismatches
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OR FILING DATE: 1999-07-29

OR APPLICATION NUMBER: JP 1999-300253

OR FILING DATE: 1999-08-27

OR APPLICATION NUMBER: JP 2000-118776

OR FILING DATE: 2000-01-11

OR APPLICATION NUMBER: JP 2000-183767
                                                                        finger domain id, E-value=0.0097,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: PRIMERS FOR SYNTHESIZ
FILE REFERENCE: 084335/0123
CURRENT APPLICATION NUMBER: US/10/917,503
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APPLICATION NUMBER: JP 2000-241899
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e 11063, Application US/10917503
tion No. US20070105122A1
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Pred.
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ISHII, SHIZUKO
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NAGAI, KEIICHI
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28.4%;
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APPLICANT: Bernstein, Jeanne
TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
FILE REFERENCE: 02/23929
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APPLICANT: Rupnow, Brent A.
APPLICANT: Webster, Kevin R.
APPLICANT: Webster, Donald
APPLICANT: Wong, Tai W.
TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
FILE REFERENCE: D0310 PCT
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                                          Length 313;
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Pred. No. 97;
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                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/567,867 CURRENT FILING DATE: 2006-01-27
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PRIOR APPLICATION NUMBER: US 60/490,890
                                                                                                                                                                                                                                                            US-10-567-867-1402; Sequence 1402, Application US/10567867; Publication No. US20070105114A1; GENERAL INFORMATION:
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Freilich, Shiri
Beck, Nili
Zhu, Wei-Yong
Wasserman, Alon
Hermesh, Chen
Azar, Idit
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SOFTWARE: Patentin version
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APPLICANT: Xie, Hanging
APPLICANT: Dahari, Dvir
; ORGANISM: Homo sapiens
US-11-443-428A-890388
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LENGTH: 614
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43 IYNDLSKNTTGSTIAEIRRLRIEIEKLQWLHQQELSEMKHNLELTMAEMRQSLEQERDRL
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43 IYNDLSKNTTGSTIAEIRRLRIEIEKLQWLHQQELSEMKHNLELTMAEMRQ
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F: Bernstein, Jeanne
INVENTION: METHODS AND SYSTEMS USEFUL, FOR ANNOTATING
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T: Bernstein, Jeanne
INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING
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Mismatches
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Pred. No. 44;
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CURRENT FILING DATE: 2006-05-31
NUMBER OF SEQ ID NOS: 1034312
                                                                                                                     Sequence 890387, Application US/11443428A Sequence 890387, Application US/11443428A Publication No. US20070083334A1 GENERAL INFORMATION:
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ID NO 890387
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Zhu, Wei-Yong
Wasserman, Alon
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Wasserman, Alor
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Dahari, Dvir
Levanon, Brez
Freilich, Shir
Beck, Nili
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: Xie, Hanging
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Levanon, Ere
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Beck, Nili
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GENERAL INFORMATION:
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; ORGANISM: Homo sapiens US-11-582-861-6676
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Publication No.
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APPLICANT: Aebersold, Rudolf H.
TITLE OF INVENTION: TISSUE- AND SERUM-DERIVED GLYCOPROTEINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
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Pred. No. 1.1e-
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CURRENT APPLICATION NUMBER: US/10/405,027
CURRENT FILING DATE: 2003-04-07
PRIOR APPLICATION NUMBER: 60/369,608
PRIOR FILING DATE: 2002-04-04
PRIOR FILING DATE: 2002-04-30
NUMBER OF SEQ ID NOS: 5810
SOFTWARE: Patentin Ver. 2.0
LENGTH: 702
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TITLE OF INVENTION: Human Secreted Proteins
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CURRENT APPLICATION NUMBER: US/11/582,861
CURRENT FILING DATE: 2006-10-17
PRIOR APPLICATION NUMBER: US 60/728,044
                                                                                                                                                                                                                                                                                                                                                      Sequence 3329, Application US/10405027 Publication No. US20070015271A1 GENERAL INFORMATION:
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Sequence 6676, Application US/11582861
Publication No. US20070099251A1
GENERAL INFORMATION:
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; OTHER INFORMATION: Xaa equals
US-10-405-027-3329
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NUMBER OF SEQ ID NOS: 1034312
SOFTWARE: PatentIn version 3.
SEQ ID NO 890383
LENGTH: 647
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llarity 28.4%;
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// ORGANISM: Homo sapiens
US-11-443-428A-890383
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ORGANISM: Homo sapiens
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CURRENT APPLICATION NUMBER: US/11/582,861

CURRENT FILING DATE: 2006-10-17

PRIOR APPLICATION NUMBER: US 60/728,044

PRIOR FILING DATE: 2005-10-17

NUMBER OF SEQ ID NOS: 14918

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6675

LENGTH: 995
PRIOR FILING DATE: 2005-10-17
NUMBER OF SEQ ID NOS: 14918
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6676
LENGTH: 764
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lon No. US20070083334A1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 6675, Application US/11582861
Publication No. US20070099251A1
GENERAL INFORMATION:
APPLICANT: Zhang, Hui
APPLICANT: Aebersold, Rudolf H.
TITLE OF INVENTION: TISSUE- AND SERUM
TITLE OF INVENTION: AND METHODS OF T
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Best Local Similarity 28.4
Matches 23; Conservative
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Hermesh, Chen
Azar, Idit
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Freilich, Shir
Beck, Nili
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Xie, Hanging
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APPLICANT: Bernstein, Jeanne
TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR SEQUENCES
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TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING BIOMOLECULAR
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837 IYNDLSKNTTGSTIAEIRRLRIEIEKLQWLHQQELSEMKHNLELTMAEMRQSLEQERDRL
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Pred. No. 1
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                                                                                                                                                        FILE REFERENCE: 02/23929
CURRENT APPLICATION NUMBER: US/11/443,428A
CURRENT FILING DATE: 2006-05-31
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1034312
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Q ID NO 890399
LENGTH: 1107
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Freilich, Sn...
Beck, Nili
Thu, Wei-Yong
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                                          Beck, Mil. Zhu, Wei-Yong
                                  Shiri
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: Xie, Hanging
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Bernstein,
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Azar, Idit
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LENGTH: 1115
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TITLE OF INVENTION: METHODS AND SYSTEMS USEFUL FOR ANNOTATING
FILE REFERENCE: 02/23929
CURRENT APPLICATION NUMBER: US/11/443,428A
CURRENT FILING DATE: 2006-05-31
NUMBER OF SEQ ID NOS: 1034312
SOFTWARE: Patentin version 3.1
SEQ ID NO 890395
LENGTH: 1072
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Pred. No. 1.9e+02;
); Mismatches 23
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    METHODS AND SYSTEMS USEFUL
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Pred. No. 1.9e.
.0; Mismatches
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US-11-443-428A-890399
; Sequence 890399, Application US/11443428A
; Publication No. US20070083334A1
; GENERAL INFORMATION:
; APPLICANT: Mintz, Liat
, appLICANT: Xie, Hanging
TITLE OF INVENTION: METHODS AND SYSTEMS USIFILE REFERENCE: 02/23929

CURRENT APPLICATION NUMBER: US/11/443,428A

CURRENT FILING DATE: 2006-05-31

NUMBER OF SEQ ID NOS: 1034312

SOFTWARE: Patentin version 3.1

SEQ ID NO 890379

LENGTH: 1072
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Wasserman, Alon
Hermesh, Chen
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, Shiri
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Xie, Hanging
Dahari, Dvir
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US-11-443-428A-890379
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Freilich, S
Beck, Nili
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